

SEQUENCE LISTING



(1) GENERAL INFORMATION:

(i) APPLICANT: STUIVER, Maarten Hendrik  
CUSTERS, Jerome Humbertina Henricus Victor  
SELA-BURLAGE, Marianne Beatrix  
MELCHERS, Leo Sjoerd  
VAN DEVENTER-TROOST, Johanna Pieternella  
LAGEWEG, Wessel  
PONSTEIN, Anne Silene  
LAGEWEG, Wessel  
PONSTEIN, Anne Silene

(ii) TITLE OF INVENTION: ANTIFUNGAL PROTEINS, DNA CODING THEREFOR,  
AND HOSTS INCORPORATING SAME.

(iii) NUMBER OF SEQUENCES: 75

(iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: LADAS & PARRY  
(B) STREET 26 WEST 61 STREET  
(C) CITY NEW YORK  
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(F) 10023 - 7604

(v) COMPUTER READABLE FORM: (A) MEDIUM TYPE: 3.25" Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: WINDOWS 95  
(D) SOFTWARE: WORDPERFECT 8

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(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 09/258,031  
(B) FILING DATE: 25-FEB-1999  
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: PCT/EP97/04923  
(B) FILING DATE: 04-SEP-1997

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: EP97200831.2  
(B) FILING DATE: 19-MAR-1997

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: EP96202466.7  
(B) FILING DATE: 04-SEP-1996

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helianthus annuus

(B) STRAIN: cv. zebulon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Ser Ile Asn Val Asp Ile Glu Gln Glu Thr Ala Trp Val Gln Ala Gly  
1 5 10 15

Ala Thr Leu Gly Glu Val Tyr Tyr Arg  
20 25

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helianthus annuus

(B) STRAIN: cv. zebulon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Asp Pro Ser Phe Pro Ile Thr Gly Glu Val Tyr Thr Pro Gly Xaa Ser  
1 5 10 15

Ser Phe Pro Thr Val Leu Gln Asn Tyr  
20 25

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

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- (ix) FEATURE:  
    (A) NAME/KEY: misc\_feature  
    (B) LOCATION: 1  
    (D) OTHER INFORMATION: /function= "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AACTTCTCCN AGNGTNGCNC CNGCTTGNA CCA

33

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 32 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: YES
- (ix) FEATURE:  
    (A) NAME/KEY: misc\_feature  
    (B) LOCATION: 1  
    (D) OTHER INFORMATION: /function= "primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GATCCNTCTT TCCCNATTAC TGGNGAGGTT TA

32

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 354 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Helianthus annuus  
    (B) STRAIN: cv. zebulon
- (ix) FEATURE:  
    (A) NAME/KEY: CDS  
    (B) LOCATION: 1..354
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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GAT CCG TCT TTC CCG ATT ACT GGG GAG GTT TAC ACT CCC GGA AAC TCA	48
Asp Pro Ser Phe Pro Ile Thr Gly Glu Val Tyr Thr Pro Gly Asn Ser	
1 5 10 15	
TCT TTT CCT ACC GTC TTG CAA AAC TAC ATC CGA AAC CTT CGG TTC AAT	96
Ser Phe Pro Thr Val Leu Gln Asn Tyr Ile Arg Asn Leu Arg Phe Asn	
20 25 30	
GAA ACT ACC ACA CCA AAA CCC TTT TTA ATC ATC ACA GCC GAA CAT GTT	144
Glu Thr Thr Thr Pro Lys Pro Phe Leu Ile Ile Thr Ala Glu His Val	
35 40 45	
TCC CAC ATT CAG GCA GCT GTG GTT TGT GGC AAA CAA AAC CGG TTG CTA	192
Ser His Ile Gln Ala Ala Val Val Cys Gly Lys Gln Asn Arg Leu Leu	
50 55 60	
CTG AAA ACC AGA AGC GGT GGT CAT GAT TAT GAA GGT CTT TCC TAC CTT	240
Leu Lys Thr Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Leu	
65 70 75 80	
ACA AAC ACA AAC CAA CCC TTC TTC ATT GTG GAC ATG TTC AAT TTA AGG	288
Thr Asn Thr Asn Gln Pro Phe Phe Ile Val Asp Met Phe Asn Leu Arg	
85 90 95	
TCC ATA AAC GTA GAT ATC GAA CAA GAA ACC GCA TGG GTC CAA GCC GGC	336
Ser Ile Asn Val Asp Ile Glu Gln Glu Thr Ala Trp Val Gln Ala Gly	
100 105 110	
GCC ACC CTC GGA GAA GTT	354
Ala Thr Leu Gly Glu Val	
115	

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Asp Pro Ser Phe Pro Ile Thr Gly Glu Val Tyr Thr Pro Gly Asn Ser	
1 5 10 15	
Ser Phe Pro Thr Val Leu Gln Asn Tyr Ile Arg Asn Leu Arg Phe Asn	
20 25 30	
Glu Thr Thr Thr Pro Lys Pro Phe Leu Ile Ile Thr Ala Glu His Val	
35 40 45	
Ser His Ile Gln Ala Ala Val Val Cys Gly Lys Gln Asn Arg Leu Leu	
50 55 60	
Leu Lys Thr Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Leu	
65 70 75 80	

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Thr Asn Thr Asn Gln Pro Phe Phe Ile Val Asp Met Phe Asn Leu Arg  
85 90 95

Ser Ile Asn Val Asp Ile Glu Gln Glu Thr Ala Trp Val Gln Ala Gly  
100 105 110

Ala Thr Leu Gly Glu Val  
115

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1
  - (D) OTHER INFORMATION: /function= "primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CAGGCAGCTG TGGTTTGTGG C

21

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1
  - (D) OTHER INFORMATION: /function= "primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GTCCACAATG AAGAAGGGTT G

21

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(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1
  - (D) OTHER INFORMATION: /function= "primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ACGTAGATAT CGAACAAGAA ACCGC

25

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GCTTTACTAC ACGGGCTTCC CCAG

24

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTGGGGAAGC CCGTGTAGTA AAGC

24

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGTACTCCAA CCACGGCGCT C

21

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CGGGAAGTTG CAGAAGATTG GGTTG

25

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GAGCAAGAGA AGAAGGAGAC

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(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helianthus annuus
- (B) STRAIN: Zebulon

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 21..1608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATATCACATC TTCTTTCAAC ATG CAA ACT TCC ATT CTT ACT CTC CTT CTT 50  
Met Gln Thr Ser Ile Leu Thr Leu Leu Leu  
1 5 10

CTC TTG CTC TCA ACC CAA TCT TCT GCA ACT TCC CGT TCC ATT ACA GAT 98  
Leu Leu Leu Ser Thr Gln Ser Ser Ala Thr Ser Arg Ser Ile Thr Asp  
15 20 25

CGC TTC ATT CAA TGT TTA CAC GAC CGG GCC GAC CCT TCA TTT CCG ATA 146  
Arg Phe Ile Gln Cys Leu His Asp Arg Ala Asp Pro Ser Phe Pro Ile  
30 35 40

ACC GGA GAG GTT TAC ACT CCC GGA AAC TCA TCT TTT CCT ACC GTC TTG 194  
Thr Gly Glu Val Tyr Thr Pro Gly Asn Ser Ser Phe Pro Thr Val Leu  
45 50 55

CAA AAC TAC ATC CGA AAC CTT CGG TTC AAT GAA ACT ACC ACA CCA AAA 242  
Gln Asn Tyr Ile Arg Asn Leu Arg Phe Asn Glu Thr Thr Thr Pro Lys  
60 65 70

CCC TTT TTA ATC ATC ACA GCC GAA CAT GTT TCC CAC ATT CAG GCA GCT 290  
Pro Phe Leu Ile Ile Thr Ala Glu His Val Ser His Ile Gln Ala Ala  
75 80 85 90

GTG GTT TGT GGC AAA CAA AAC CGG TTG CTA CTG AAA ACC AGA AGC GGT 338  
Val Val Cys Gly Lys Gln Asn Arg Leu Leu Leu Lys Thr Arg Ser Gly  
95 100 105

GGT CAT GAT TAT GAA GGT CTT TCC TAC CTT ACA AAC ACA AAC CAA CCC 386  
Gly His Asp Tyr Glu Gly Leu Ser Tyr Leu Thr Asn Thr Asn Gln Pro  
110 115 120

TTC TTC ATT GTG GAC ATG TTC AAT TTA AGG TCC ATA AAC GTA GAT ATC 434  
Phe Phe Ile Val Asp Met Phe Asn Leu Arg Ser Ile Asn Val Asp Ile  
125 130 135

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GAA CAA GAA ACC GCA TGG GTC CAA GCC GGT GCG ACT CTT GGT GAA GTG	482
Glu Gln Glu Thr Ala Trp Val Gln Ala Gly Ala Thr Leu Gly Glu Val	
140 145 150	
TAC TAT CGA ATA GCG GAG AAA AGT AAC AAG CAT GGT TTT CCG GCA GGG	530
Tyr Tyr Arg Ile Ala Glu Lys Ser Asn Lys His Gly Phe Pro Ala Gly	
155 160 165 170	
GTT TGT CCA ACG GTT GGC GTT GGT GGG CAT TTT AGT GGT GGT GGG TAT	578
Val Cys Pro Thr Val Gly Val Gly Gly His Phe Ser Gly Gly Gly Tyr	
175 180 185	
GGT AAT TTG ATG AGA AAA TAT GGT TTG TCG GTT GAT AAT ATT GTT GAT	626
Gly Asn Leu Met Arg Lys Tyr Gly Leu Ser Val Asp Asn Ile Val Asp	
190 195 200	
GCT CAA ATA ATA GAT GTG AAT GGC AAG CTT TTG GAT CGA AAG AGT ATG	674
Ala Gln Ile Ile Asp Val Asn Gly Lys Leu Leu Asp Arg Lys Ser Met	
205 210 215	
GGT GAG GAT TTG TTT TGG GCG ATC ACC GGC GGT GGT GGT GTT AGT TTT	722
Gly Glu Asp Leu Phe Trp Ala Ile Thr Gly Gly Gly Val Ser Phe	
220 225 230	
GGT GTG GTT CTA GCC TAC AAA ATC AAA CTA GTT CGT GTT CCG GAG GTT	770
Gly Val Val Leu Ala Tyr Lys Ile Lys Leu Val Arg Val Pro Glu Val	
235 240 245 250	
GTG ACC GTG TTT ACC ATT GAA AGA AGA GAG GAA CAA AAC CTC AGC ACC	818
Val Thr Val Phe Thr Ile Glu Arg Arg Glu Glu Gln Asn Leu Ser Thr	
255 260 265	
ATC GCG GAA CGA TGG GTA CAA GTT GCT GAT AAG CTA GAT AGA GAT CTT	866
Ile Ala Glu Arg Trp Val Gln Val Ala Asp Lys Leu Asp Arg Asp Leu	
270 275 280	
TTC CTT CGA ATG ACC TTT AGT GTC ATA AAC GAT ACC AAC GGT GGA AAG	914
Phe Leu Arg Met Thr Phe Ser Val Ile Asn Asp Thr Asn Gly Gly Lys	
285 290 295	
ACA GTC CGT GCT ATC TTT CCA ACG TTG TAC CTT GGA AAC TCG AGG AAT	962
Thr Val Arg Ala Ile Phe Pro Thr Leu Tyr Leu Gly Asn Ser Arg Asn	
300 305 310	
CTT GTT ACA CTT TTG AAT AAA GAT TTC CCC GAG TTA GGG TTG CAA GAA	1010
Leu Val Thr Leu Leu Asn Lys Asp Phe Pro Glu Leu Gly Leu Gln Glu	
315 320 325 330	
TCG GAT TGT ACT GAA ATG AGT TGG GTT GAG TCT GTG CTT TAC TAC ACG	1058
Ser Asp Cys Thr Glu Met Ser Trp Val Glu Ser Val Leu Tyr Tyr Thr	
335 340 345	
GGC TTC CCC AGT GGT ACT CCA ACC ACG GCG CTC TTA AGC CGT ACT CCT	1106
Gly Phe Pro Ser Gly Thr Pro Thr Thr Ala Leu Leu Ser Arg Thr Pro	
350 355 360	

Cont.

CAA AGA CTC AAC CCA TTC AAG ATC AAA TCC GAT TAT GTG CAA AAT CCT 1154  
Gln Arg Leu Asn Pro Phe Lys Ile Lys Ser Asp Tyr Val Gln Asn Pro  
365 370 375

ATT TCT AAA CGA CAG TTC GAG TTC ATC TTC GAA AGG CTG AAA GAA CTT 1202  
Ile Ser Lys Arg Gln Phe Glu Phe Ile Phe Glu Arg Leu Lys Glu Leu  
380 385 390

GAA AAC CAA ATG TTG GCT TTC AAC CCA TAT GGT GGT AGA ATG AGT GAA 1250  
Glu Asn Gln Met Leu Ala Phe Asn Pro Tyr Gly Gly Arg Met Ser Glu  
395 400 405 410

ATA TCC GAA TTC GCA AAG CCT TTC CCA CAT AGA TCG GGT AAC ATA GCG 1298  
Ile Ser Glu Phe Ala Lys Pro Phe Pro His Arg Ser Gly Asn Ile Ala  
415 420 425

AAA ATT CAA TAC GAA GTA AAC TGG GAG GAT CTT AGC GAT GAA GCC GAA 1346  
Lys Ile Gln Tyr Glu Val Asn Trp Glu Asp Leu Ser Asp Glu Ala Glu  
430 435 440

AAT CGT TAC TTG AAT TTC ACA AGG CTG ATG TAT GAT TAC ATG ACC CCA 1394  
Asn Arg Tyr Leu Asn Phe Thr Arg Leu Met Tyr Asp Tyr Met Thr Pro  
445 450 455

TTT GTG TCG AAA AAC CCT AGA AAA GCA TTT TTG AAC TAT AGG GAT TTG 1442  
Phe Val Ser Lys Asn Pro Arg Lys Ala Phe Leu Asn Tyr Arg Asp Leu  
460 465 470

GAT ATT GGT ATC AAC AGC CAT GGC AGG AAT GCT TAT ACT GAA GGA ATG 1490  
Asp Ile Gly Ile Asn Ser His Gly Arg Asn Ala Tyr Thr Glu Gly Met  
475 480 485 490

GTT TAT GGG CAC AAG TAT TTC AAA GAG ACA AAT TAC AAG AGG CTA GTA 1538  
Val Tyr Gly His Lys Tyr Phe Lys Glu Thr Asn Tyr Lys Arg Leu Val  
495 500 505

AGT GTG AAG ACT AAA GTT GAT CCT GAC AAC TTC TTT AGG AAT GAG CAA 1586  
Ser Val Lys Thr Lys Val Asp Pro Asp Asn Phe Phe Arg Asn Glu Gln  
510 515 520

AGC ATC CCA ACT TTG TCA TCT T GAAGAACGTA CATATATAAA TAAATACCTT 1638  
Ser Ile Pro Thr Leu Ser Ser  
525

TGTGCATGGT ATTTTCAGGG TGTAAAGTG ATATTCAGAT ATTTATGATA GAATTTTGAC 1698

TTGTATTTTA TACAATCAAA ATTGTATGGT TCTCCGAATT TCTCTTTTTA ATTCTGAAAA 1758

ATACATATTA GTATTGTCAA AAAAAA 1784

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 529 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Gln Thr Ser Ile Leu Thr Leu Leu Leu Leu Leu Ser Thr Gln  
1 5 10 15  
Ser Ser Ala Thr Ser Arg Ser Ile Thr Asp Arg Phe Ile Gln Cys Leu  
20 25 30  
His Asp Arg Ala Asp Pro Ser Phe Pro Ile Thr Gly Glu Val Tyr Thr  
35 40 45  
Pro Gly Asn Ser Ser Phe Pro Thr Val Leu Gln Asn Tyr Ile Arg Asn  
50 55 60  
Leu Arg Phe Asn Glu Thr Thr Thr Pro Lys Pro Phe Leu Ile Ile Thr  
65 70 75 80  
Ala Glu His Val Ser His Ile Gln Ala Ala Val Val Cys Gly Lys Gln  
85 90 95  
Asn Arg Leu Leu Leu Lys Thr Arg Ser Gly Gly His Asp Tyr Glu Gly  
100 105 110  
Leu Ser Tyr Leu Thr Asn Thr Asn Gln Pro Phe Phe Ile Val Asp Met  
115 120 125  
Phe Asn Leu Arg Ser Ile Asn Val Asp Ile Glu Gln Glu Thr Ala Trp  
130 135 140  
Val Gln Ala Gly Ala Thr Leu Gly Glu Val Tyr Tyr Arg Ile Ala Glu  
145 150 155 160  
Lys Ser Asn Lys His Gly Phe Pro Ala Gly Val Cys Pro Thr Val Gly  
165 170 175  
Val Gly Gly His Phe Ser Gly Gly Gly Tyr Gly Asn Leu Met Arg Lys  
180 185 190  
Tyr Gly Leu Ser Val Asp Asn Ile Val Asp Ala Gln Ile Ile Asp Val  
195 200 205  
Asn Gly Lys Leu Leu Asp Arg Lys Ser Met Gly Glu Asp Leu Phe Trp  
210 215 220  
Ala Ile Thr Gly Gly Gly Gly Val Ser Phe Gly Val Val Leu Ala Tyr  
225 230 235 240  
Lys Ile Lys Leu Val Arg Val Pro Glu Val Val Thr Val Phe Thr Ile  
245 250 255  
Glu Arg Arg Glu Glu Gln Asn Leu Ser Thr Ile Ala Glu Arg Trp Val  
260 265 270  
Gln Val Ala Asp Lys Leu Asp Arg Asp Leu Phe Leu Arg Met Thr Phe  
275 280 285

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Ser Val Ile Asn Asp Thr Asn Gly Gly Lys Thr Val Arg Ala Ile Phe  
 290 295 300  
 Pro Thr Leu Tyr Leu Gly Asn Ser Arg Asn Leu Val Thr Leu Leu Asn  
 305 310 315 320  
 Lys Asp Phe Pro Glu Leu Gly Leu Gln Glu Ser Asp Cys Thr Glu Met  
 325 330 335  
 Ser Trp Val Glu Ser Val Leu Tyr Tyr Thr Gly Phe Pro Ser Gly Thr  
 340 345 350  
 Pro Thr Thr Ala Leu Leu Ser Arg Thr Pro Gln Arg Leu Asn Pro Phe  
 355 360 365  
 Lys Ile Lys Ser Asp Tyr Val Gln Asn Pro Ile Ser Lys Arg Gln Phe  
 370 375 380  
 Glu Phe Ile Phe Glu Arg Leu Lys Glu Leu Glu Asn Gln Met Leu Ala  
 385 390 395 400  
 Phe Asn Pro Tyr Gly Gly Arg Met Ser Glu Ile Ser Glu Phe Ala Lys  
 405 410 415  
 Pro Phe Pro His Arg Ser Gly Asn Ile Ala Lys Ile Gln Tyr Glu Val  
 420 425 430  
 Asn Trp Glu Asp Leu Ser Asp Glu Ala Glu Asn Arg Tyr Leu Asn Phe  
 435 440 445  
 Thr Arg Leu Met Tyr Asp Tyr Met Thr Pro Phe Val Ser Lys Asn Pro  
 450 455 460  
 Arg Lys Ala Phe Leu Asn Tyr Arg Asp Leu Asp Ile Gly Ile Asn Ser  
 465 470 475 480  
 His Gly Arg Asn Ala Tyr Thr Glu Gly Met Val Tyr Gly His Lys Tyr  
 485 490 495  
 Phe Lys Glu Thr Asn Tyr Lys Arg Leu Val Ser Val Lys Thr Lys Val  
 500 505 510  
 Asp Pro Asp Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro Thr Leu Ser  
 515 520 525

Ser

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CCGCCATGGA GACTTCCATT CTTACTC

27

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GCCGGATCCT CAAGATGACA AAGTTGGGAT GCT

33

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1589 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helianthus annuus

(B) STRAIN: Zebulon

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATG GAG ACT TCC ATT CTT ACT CTC CTT CTT CTC TTG CTC TCA ACC CAA  
Met Glu Thr Ser Ile Leu Thr Leu Leu Leu Leu Leu Ser Thr Gln  
1 5 10 15

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TCT	TCT	GCA	ACT	TCC	CGT	TCC	ATT	ACA	GAT	CGC	TTC	ATT	CAA	TGT	TTA	96
Ser	Ser	Ala	Thr	Ser	Arg	Ser	Ile	Thr	Asp	Arg	Phe	Ile	Gln	Cys	Leu	
		20						25					30			
CAC	GAC	CGG	GCC	GAC	CCT	TCA	TTT	CCG	ATA	ACC	GGA	GAG	GTT	TAC	ACT	144
His	Asp	Arg	Ala	Asp	Pro	Ser	Phe	Pro	Ile	Thr	Gly	Glu	Val	Tyr	Thr	
		35					40					45				
CCC	GGA	AAC	TCA	TCT	TTT	CCT	ACC	GTC	TTG	CAA	AAC	TAC	ATC	CGA	AAC	192
Pro	Gly	Asn	Ser	Ser	Phe	Pro	Thr	Val	Leu	Gln	Asn	Tyr	Ile	Arg	Asn	
	50					55					60					
CTT	CGG	TTC	AAT	GAA	ACT	ACC	ACA	CCA	AAA	CCC	TTT	TTA	ATC	ATC	ACA	240
Leu	Arg	Phe	Asn	Glu	Thr	Thr	Thr	Pro	Lys	Pro	Phe	Leu	Ile	Ile	Thr	
	65				70					75					80	
GCC	GAA	CAT	GTT	TCC	CAC	ATT	CAG	GCA	GCT	GTG	GTT	TGT	GGC	AAA	CAA	288
Ala	Glu	His	Val	Ser	His	Ile	Gln	Ala	Ala	Val	Val	Cys	Gly	Lys	Gln	
				85				90						95		
AAC	CGG	TTG	CTA	CTG	AAA	ACC	AGA	AGC	GGT	GGT	CAT	GAT	TAT	GAA	GGT	336
Asn	Arg	Leu	Leu	Leu	Lys	Thr	Arg	Ser	Gly	Gly	His	Asp	Tyr	Glu	Gly	
		100						105					110			
CTT	TCC	TAC	CTT	ACA	AAC	ACA	AAC	CAA	CCC	TTC	TTC	ATT	GTG	GAC	ATG	384
Leu	Ser	Tyr	Leu	Thr	Asn	Thr	Asn	Gln	Pro	Phe	Phe	Ile	Val	Asp	Met	
		115					120						125			
TTC	AAT	TTA	AGG	TCC	ATA	AAC	GTA	GAT	ATC	GAA	CAA	GAA	ACC	GCA	TGG	432
Phe	Asn	Leu	Arg	Ser	Ile	Asn	Val	Asp	Ile	Glu	Gln	Glu	Thr	Ala	Trp	
	130					135					140					
GTC	CAA	GCC	GGT	GCG	ACT	CTT	GGT	GAA	GTG	TAC	TAT	CGA	ATA	GCG	GAG	480
Val	Gln	Ala	Gly	Ala	Thr	Leu	Gly	Glu	Val	Tyr	Tyr	Arg	Ile	Ala	Glu	
	145				150					155					160	
AAA	AGT	AAC	AAG	CAT	GGT	TTT	CCG	GCA	GGG	GTT	TGT	CCA	ACG	GTT	GGC	528
Lys	Ser	Asn	Lys	His	Gly	Phe	Pro	Ala	Gly	Val	Cys	Pro	Thr	Val	Gly	
				165				170						175		
GTT	GGT	GGG	CAT	TTT	AGT	GGT	GGT	GGG	TAT	GGT	AAT	TTG	ATG	AGA	AAA	576
Val	Gly	Gly	His	Phe	Ser	Gly	Gly	Gly	Tyr	Gly	Asn	Leu	Met	Arg	Lys	
			180					185					190			
TAT	GGT	TTG	TCG	GTT	GAT	AAT	ATT	GTT	GAT	GCT	CAA	ATA	ATA	GAT	GTG	624
Tyr	Gly	Leu	Ser	Val	Asp	Asn	Ile	Val	Asp	Ala	Gln	Ile	Ile	Asp	Val	
		195					200					205				
AAT	GGC	AAG	CTT	TTG	GAT	CGA	AAG	AGT	ATG	GGT	GAG	GAT	TTG	TTT	TGG	672
Asn	Gly	Lys	Leu	Leu	Asp	Arg	Lys	Ser	Met	Gly	Glu	Asp	Leu	Phe	Trp	
	210						215				220					
GCG	ATC	ACC	GGC	GGT	GGT	GGT	GTT	AGT	TTT	GGT	GTG	GTT	CTA	GCC	TAC	720
Ala	Ile	Thr	Gly	Gly	Gly	Gly	Val	Ser	Phe	Gly	Val	Val	Leu	Ala	Tyr	
	225				230					235					240	

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AAA	ATC	AAA	CTA	GTT	CGT	GTT	CCG	GAG	GTT	GTG	ACC	GTG	TTT	ACC	ATT	768
Lys	Ile	Lys	Leu	Val	Arg	Val	Pro	Glu	Val	Val	Thr	Val	Phe	Thr	Ile	
				245					250					255		
GAA	AGA	AGA	GAG	GAA	CAA	AAC	CTC	AGC	ACC	ATC	GCG	GAA	CGA	TGG	GTA	816
Glu	Arg	Arg	Glu	Gln	Asn	Leu	Ser	Thr	Ile	Ala	Glu	Arg	Trp	Val		
			260					265					270			
CAA	GTT	GCT	GAT	AAG	CTA	GAT	AGA	GAT	CTT	TTC	CTT	CGA	ATG	ACC	TTT	864
Gln	Val	Ala	Asp	Lys	Leu	Asp	Arg	Asp	Leu	Phe	Leu	Arg	Met	Thr	Phe	
		275					280						285			
AGT	GTC	ATA	AAC	GAT	ACC	AAC	GGT	GGA	AAG	ACA	GTC	CGT	GCT	ATC	TTT	912
Ser	Val	Ile	Asn	Asp	Thr	Asn	Gly	Gly	Lys	Thr	Val	Arg	Ala	Ile	Phe	
	290					295					300					
CCA	ACG	TTG	TAC	CTT	GGA	AAC	TCG	AGG	AAT	CTT	GTT	ACA	CTT	TTG	AAT	960
Pro	Thr	Leu	Tyr	Leu	Gly	Asn	Ser	Arg	Asn	Leu	Val	Thr	Leu	Leu	Asn	
305					310					315					320	
AAA	GAT	TTC	CCC	GAG	TTA	GGG	TTG	CAA	GAA	TCG	GAT	TGT	ACT	GAA	ATG	1008
Lys	Asp	Phe	Pro	Glu	Leu	Gly	Leu	Gln	Glu	Ser	Asp	Cys	Thr	Glu	Met	
			325						330					335		
AGT	TGG	GTT	GAG	TCT	GTG	CTT	TAC	TAC	ACG	GGC	TTC	CCC	AGT	GGT	ACT	1056
Ser	Trp	Val	Glu	Ser	Val	Leu	Tyr	Tyr	Thr	Gly	Phe	Pro	Ser	Gly	Thr	
		340						345					350			
CCA	ACC	ACG	GCG	CTC	TTA	AGC	CGT	ACT	CCT	CAA	AGA	CTC	AAC	CCA	TTC	1104
Pro	Thr	Thr	Ala	Leu	Leu	Ser	Arg	Thr	Pro	Gln	Arg	Leu	Asn	Pro	Phe	
		355					360						365			
AAG	ATC	AAA	TCC	GAT	TAT	GTG	CAA	AAT	CCT	ATT	TCT	AAA	CGA	CAG	TTC	1152
Lys	Ile	Lys	Ser	Asp	Tyr	Val	Gln	Asn	Pro	Ile	Ser	Lys	Arg	Gln	Phe	
	370					375					380					
GAG	TTC	ATC	TTC	GAA	AGG	ATG	AAA	GAA	CTT	GAA	AAC	CAA	ATG	TTG	GCG	1200
Glu	Phe	Ile	Phe	Glu	Arg	Met	Lys	Glu	Leu	Glu	Asn	Gln	Met	Leu	Ala	
385				390						395				400		
TTC	AAC	CCA	TAT	GGT	GGT	AGA	ATG	AGT	GAA	ATA	TCC	GAA	TTC	GCA	AAG	1248
Phe	Asn	Pro	Tyr	Gly	Gly	Arg	Met	Ser	Glu	Ile	Ser	Glu	Phe	Ala	Lys	
			405						410					415		
CCT	TTC	CCA	CAT	AGA	TCG	GGT	AAC	ATA	GCG	AAG	ATT	CAA	TAC	GAA	GTA	1296
Pro	Phe	Pro	His	Arg	Ser	Gly	Asn	Ile	Ala	Lys	Ile	Gln	Tyr	Glu	Val	
		420						425					430			
AAC	TGG	GAG	GAT	CTT	AGC	GAT	GAA	GCC	GAA	AAT	CGT	TAC	TTG	AAT	TTC	1344
Asn	Trp	Glu	Asp	Leu	Ser	Asp	Glu	Ala	Glu	Asn	Arg	Tyr	Leu	Asn	Phe	
		435					440					445				
ACA	AGG	CTG	ATG	TAT	GAT	TAC	ATG	ACT	CCA	TTT	GTG	TCG	AAA	AAC	CCT	1392
Thr	Arg	Leu	Met	Tyr	Asp	Tyr	Met	Thr	Pro	Phe	Val	Ser	Lys	Asn	Pro	
	450					455					460					

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AGA	GAA	GCA	TTT	TTG	AAC	TAT	AGG	GAT	TTG	GAT	ATT	GGT	ATC	AAC	AGC	1440
Arg	Glu	Ala	Phe	Leu	Asn	Tyr	Arg	Asp	Leu	Asp	Ile	Gly	Ile	Asn	Ser	
465					470				475					480		
CAT	GGC	AGG	AAT	GCT	TAT	ACT	GAA	GGA	ATG	GTT	TAT	GGG	CAC	AAA	TAT	1488
His	Gly	Arg	Asn	Ala	Tyr	Thr	Glu	Gly	Met	Val	Tyr	Gly	His	Lys	Tyr	
			485						490					495		
TTC	AAA	GAG	ACA	AAT	TAC	AAG	AGG	CTA	GTA	AGT	GTG	AAG	ACT	AAA	GTT	1536
Phe	Lys	Glu	Thr	Asn	Tyr	Lys	Arg	Leu	Val	Ser	Val	Lys	Thr	Lys	Val	
			500					505					510			
GAT	CCT	GAC	AAC	TTC	TTT	AGG	AAT	GAG	CAA	AGC	ATC	CCA	ACT	TTG	TCA	1584
Asp	Pro	Asp	Asn	Phe	Phe	Arg	Asn	Glu	Gln	Ser	Ile	Pro	Thr	Leu	Ser	
		515					520					525				
TCT	TG															1589
Ser																
	530															

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 529 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Met	Glu	Thr	Ser	Ile	Leu	Thr	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Thr	Gln	
1				5				10						15		
Ser	Ser	Ala	Thr	Ser	Arg	Ser	Ile	Thr	Asp	Arg	Phe	Ile	Gln	Cys	Leu	
		20						25					30			
His	Asp	Arg	Ala	Asp	Pro	Ser	Phe	Pro	Ile	Thr	Gly	Glu	Val	Tyr	Thr	
		35					40					45				
Pro	Gly	Asn	Ser	Ser	Phe	Pro	Thr	Val	Leu	Gln	Asn	Tyr	Ile	Arg	Asn	
	50					55					60					
Leu	Arg	Phe	Asn	Glu	Thr	Thr	Thr	Pro	Lys	Pro	Phe	Leu	Ile	Ile	Thr	
65				70					75					80		
Ala	Glu	His	Val	Ser	His	Ile	Gln	Ala	Ala	Val	Val	Cys	Gly	Lys	Gln	
			85					90					95			
Asn	Arg	Leu	Leu	Leu	Lys	Thr	Arg	Ser	Gly	Gly	His	Asp	Tyr	Glu	Gly	
		100						105					110			
Leu	Ser	Tyr	Leu	Thr	Asn	Thr	Asn	Gln	Pro	Phe	Phe	Ile	Val	Asp	Met	
		115				120						125				
Phe	Asn	Leu	Arg	Ser	Ile	Asn	Val	Asp	Ile	Glu	Gln	Glu	Thr	Ala	Trp	
	130					135						140				

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Cont.



Val	Gln	Ala	Gly	Ala	Thr	Leu	Gly	Glu	Val	Tyr	Tyr	Arg	Ile	Ala	Glu	145	150	155	160
Lys	Ser	Asn	Lys	His	Gly	Phe	Pro	Ala	Gly	Val	Cys	Pro	Thr	Val	Gly	165	170	175	
Val	Gly	Gly	His	Phe	Ser	Gly	Gly	Gly	Tyr	Gly	Asn	Leu	Met	Arg	Lys	180	185	190	
Tyr	Gly	Leu	Ser	Val	Asp	Asn	Ile	Val	Asp	Ala	Gln	Ile	Ile	Asp	Val	195	200	205	
Asn	Gly	Lys	Leu	Leu	Asp	Arg	Lys	Ser	Met	Gly	Glu	Asp	Leu	Phe	Trp	210	215	220	
Ala	Ile	Thr	Gly	Gly	Gly	Gly	Val	Ser	Phe	Gly	Val	Val	Leu	Ala	Tyr	225	230	235	240
Lys	Ile	Lys	Leu	Val	Arg	Val	Pro	Glu	Val	Val	Thr	Val	Phe	Thr	Ile	245	250	255	
Glu	Arg	Arg	Glu	Glu	Gln	Asn	Leu	Ser	Thr	Ile	Ala	Glu	Arg	Trp	Val	260	265	270	
Gln	Val	Ala	Asp	Lys	Leu	Asp	Arg	Asp	Leu	Phe	Leu	Arg	Met	Thr	Phe	275	280	285	
Ser	Val	Ile	Asn	Asp	Thr	Asn	Gly	Gly	Lys	Thr	Val	Arg	Ala	Ile	Phe	290	295	300	
Pro	Thr	Leu	Tyr	Leu	Gly	Asn	Ser	Arg	Asn	Leu	Val	Thr	Leu	Leu	Asn	305	310	315	320
Lys	Asp	Phe	Pro	Glu	Leu	Gly	Leu	Gln	Glu	Ser	Asp	Cys	Thr	Glu	Met	325	330	335	
Ser	Trp	Val	Glu	Ser	Val	Leu	Tyr	Tyr	Thr	Gly	Phe	Pro	Ser	Gly	Thr	340	345	350	
Pro	Thr	Thr	Ala	Leu	Leu	Ser	Arg	Thr	Pro	Gln	Arg	Leu	Asn	Pro	Phe	355	360	365	
Lys	Ile	Lys	Ser	Asp	Tyr	Val	Gln	Asn	Pro	Ile	Ser	Lys	Arg	Gln	Phe	370	375	380	
Glu	Phe	Ile	Phe	Glu	Arg	Met	Lys	Glu	Leu	Glu	Asn	Gln	Met	Leu	Ala	385	390	395	400
Phe	Asn	Pro	Tyr	Gly	Gly	Arg	Met	Ser	Glu	Ile	Ser	Glu	Phe	Ala	Lys	405	410	415	
Pro	Phe	Pro	His	Arg	Ser	Gly	Asn	Ile	Ala	Lys	Ile	Gln	Tyr	Glu	Val	420	425	430	
Asn	Trp	Glu	Asp	Leu	Ser	Asp	Glu	Ala	Glu	Asn	Arg	Tyr	Leu	Asn	Phe	435	440	445	

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cont.

Thr Arg Leu Met Tyr Asp Tyr Met Thr Pro Phe Val Ser Lys Asn Pro  
450 455 460

Arg Glu Ala Phe Leu Asn Tyr Arg Asp Leu Asp Ile Gly Ile Asn Ser  
465 470 475 480

His Gly Arg Asn Ala Tyr Thr Glu Gly Met Val Tyr Gly His Lys Tyr  
485 490 495

Phe Lys Glu Thr Asn Tyr Lys Arg Leu Val Ser Val Lys Thr Lys Val  
500 505 510

Asp Pro Asp Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro Thr Leu Ser  
515 520 525

Ser

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GAGAAACTCG GAGACTTTCA CACAATGCCT AACCTCAAAC TCCGACCCCA AACATCCCAT 60  
CTCCCCCGCT ATCTTCTTCT CCGGAAATGG CTCCTACTCC TCCGTATTAC AAGCCAACAT 120  
CCGTAACCTC CGCTTCAACA CCACCTCAAC TCCGAAACCC TTCCTCATAA TCGCCGCAAC 180  
ACATGAATCC CATGTGCAAG CCGCGATTAC TTGCGGGAAA CGCCACAACC TTCAGATGAA 240  
AATCAGAAGT GGAGGCCACG ACTACGATGG CTTGTCATAC GTTACATACT CTGGCAAACC 300  
GTTCTTCGTC CTCGACATGT TTAACCTCCG TTCGGTGGAT GTCGACGTGG 350

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs

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cont

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GGCATGGATC TCCGCCGAG CGACTCTCGG AGAGGTTTAT TATCGGATTT GGGAGAAAAG 60  
CAGAGTCCAT GGATTCCCCG CCGGAGTTTG ACCGACGGTT GGTGTTGGTG GGCATTTAAG 120  
CGGCGGTGGT TACGGTAACA TGGTGAGGAA GTTTGGATTA TCTGTGGATT ACGTTGAGGA 180  
TGCCAAGATC GTCGATGTAA ACNGTCGGGT TTAGATCGG AAAGCAATGG GTGAGGATCT 240  
GTTCTGGGCG ATTACCGGTG GAGGAGGAGG TAGCGTAC 278

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TGGACATATT AGCGGAGGAG GATTCCGTAC AATAATGAGG AAATACGGTT TAGCGTCTGA 60  
TAACGTTGTG GACGCACGTT TGATGGATGT AAATGGGAAA ACTCTTGACC GGAAAACGAT 120

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GGGAGAGGAT TTGTTTTGGG CGCTTAGAGG CGGTGGAGCT GCGAGTTTTG GCGTTGTCTT 180  
 GTCGTGGAAG GTTAAGCTTG CTAGGGTTCC TGAAAAGGTA ACTTGTTTCA TAAGTCAACA 240  
 TCCGATGGGA CCTAGCATGA ACAAGCTTGT TCATAGATGG CAATCCATAG GATCAAGANN 300  
 GCTAGACGAA GATTTATTCA TCAGAGTCAA TATTGACAAC AGTCT 345

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GTTTCGTAAAC ACCTATCCTN NANGGGCNAA AGNATATCAA AGNTTGNTTA NGNAACCCAA 60  
 NATTTCTGAA CTGGCCNCCT TCGGTGGTAT ATGNCNAAAN CCCTTGAATC TGCGNANCCN 120  
 ATTCCGCATA GAAACGGAAC CCTCTTCAAG ATTCTCTATT TACNCGAACT GNCTAGANNG 180  
 AATGACAAGA CATCGAGTAG NAAAATCAAC TGGATCAAAG AGATATACAA TTACATGGCG 240  
 CCTTATGTCT CAAGCAATCC AAGACAAGCA TATGTGAACT ACAGAGATCT AGACTTCGGA 300  
 CAGAACAAGA ACAACGCAAA GGTAACTTC ATTGAAGCTA AAATCTGGGG ACCTAAGTAC 360  
 TTCAAAGGCA ATTTTGACAG ATTGGTGAAG ATTAAAACCA AGGTTGATCC AGAGAACTTC 420  
 TTCAGGCACG AGCAGAGTAT CCCACCTATG CCCTACTAGA AGCTAGGTTC ATGAAACCAA 480  
 TAACATTATC AAAAATAAGR ATAAATGRTA ATTGTATACA ACATGATTCG KCTTTCTTTA 540  
 TTCAGACAA TGTGGACACT ACTCTAAANT AAAAWGTCNA TTTACCTTAA AAAAAAATA 600  
 ATCCCNNTA ANANAAAANT GGGGGGGCCN TTTTGGGGN TCCCGGTTTT NGGACGGGGN 660  
 GCTTTNGGGG GGCTTGGNNT TTTTTTNGGN GCCCC 695

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(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TCTGTTTTNA GGCAGAGCAG AGGAAGTTGT TGCTTTGCTT GGTAAGGAGT TTCCTGAATT 60  
NAGTTTAAAG AAGGAGAACT GTTCGGAGAT GACTTGGTTT CAGTCAGCTT TATGGTGGGA 120  
TAATCGTGTT AACCTACTC ANATTGATCC WAAAGTGTTT CTCGATCGGA ATCTTGATAG 180  
AGCGAATTTT GGAAAGAGGA AATCGGATTA CGTTGCGAGT AAGATTCCTA GAGATGGGAT 240  
TAAGYCTTTT TCCAAGARGA TGMCTGACCT GGGGAAAAYC GGGCTTGTTT TTAAWCCGTA 300  
TG GTGGGAAA ATGGCGGAGG TTACGGTTAA CGCGACGCCG TTTCCNCACC GAAGCAAGCT 360  
TTTTAAGATT CAGTACTCGG TGA CT TNGCA AGAAACTCT NTCGAGATAG AGAAAGGGTT 420  
TCTTGAATCA GGCTAACGTC CTTATAGGTT CATGACCGGG TTTT TNAGCA AGANCCCTGG 480  
AATNCTTACT TNAAT 495

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana  
(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

AAATTTAAAC AAATCAATGT TGATATTGAA TCCAATAGTG CTTGGTTTCA ACCTGGTGCT 60  
ACGCTTGGTG AGCTTTACTA CAGAATTNCA GAGAAGAGCA AAATCCATGG ATTTCCNGCG 120  
GGTTTNTNCA CAAGCNTAGG CATAGGTGGG TATATNANAG GCGGTGGATA CGGTACCTTG 180  
ATGAGGAAGT ATGGTCTTNC GGGA 204

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana  
(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 2..491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GAGATTTCTC GAGCAAGATA CTCCACTGAT GATCTTTGAG CCATTGGGTG GGAAAATCAG 60  
CAAGATTTCA GAAACAGAAT CTCCATATCC ACACAGAAGA GGTAATCTGT ATAATATACA 120  
GTACATGGTG AAATGGAAAG TGAATGANGT CGAGGAGATG AACAAACATG TCAGGTGGAT 180  
GAGATCGTTA CACGATTACA TGACTCCGTA TGTTTCTAAA TCGCCGAGAG GAGCTTATTT 240  
GANTTACAGA GATCTTGATT TGGGCTCGAC CAAAGGGATT AACACGGGTT TCGGAGATGC 300  
AAGGAAATGG NNGGGTGAGN CTTTTTTTCAA AGGTAATTTT CAAGGGGTTA GGTTTTGGTT 360  
AAAGGGGAGG TTTNNCCCAN CAAATTTTTT TTCAGGANCC GGCCANGNTT TTCCCCCCCC 420  
TNTTTTTNGG NCCCCAATCN AAANCCCCGT TTAAAAGGG GGGCCATTTT NTTTTTTNCA 480

## (2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 407 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Arabidopsis thaliana
  - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 3..407

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

ATTGTGTCGT GAGGTAACT TTGACTTTAG TCAACGGTAC GAAGCCTGGT GAGAATACGG 60  
TTTTCGCGAC TTTCATTGGG ATGTATTTAG GCCGGTCGGA TAAGCTGTTG ACCGTNATGA 120  
ACCGGGATTT CCCGGAGTTG AAGCTGAAGA AAACCGATTN TACCGAGATG AGATGGATCG 180  
ATTCGTTTCT GTTTTGGGAC GATTATCCGG TTGGTACACC GACTTCTGTG CTACTAAATC 240  
CGCTAGTCGC AAAAAAGTTG TTCATGAAAC GAAAATCGGA CTACGTGAAG CGTCTNATTT 300  
TCGAGAACCC GATCTCNNGT TTGATACTCA AGAAATTTGT AGAGGTTNNG AAAGTTAAAA 360  
TNAATTTGGA TCCGCATTNN GGNANNNATG GTGAAACCCC NNGTTNT 407

## (2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 360 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Arabidopsis thaliana

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Cont.

(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ACGGCGTCGT ATTGGCCTAC AAAATAAACC TTGTTGAAGT CCCAGAAAAC GTCACCGTTT 60  
TCAGAATCTC CCGGACGTTA GAACAAAATG CGACGGATAT CATTACCGG TGGCAACAAG 120  
TTGCACCGAA GCTTCCCGAC GAGCTTTTCA TAAGANCAGT CATTGACGTA NAAACGGCAC 180  
TGTTTCATNN CTCAAAGAC CGTCAGACAA CATTCATAGC AATGTTTCTA GGAGACACGN 240  
CAACTCTACT GTCGATATTA AACCGGAGAT TCCCAGAATT GGGTTTGGTC CGGTCTGACT 300  
GTACCGNAAC AAGCNNTTGG ATCCAATCTG TGCTATTTTT GGGACAAATA TCCCAGGTTG 360

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TCTTCACTGT CACCAAAACG TTAGAACAAG ACGCAAGATT GAAGACTATT TCTAAGTGGC 60  
AACAAATTTT ATCCAAGATT ATTGAAGAGA TACACATCCG AGTGGTACTC AGAGCAGCTG 120  
GAAATGATGG AAACAAGACT GTGACAATGA CCTACCTAGG TCAGTTTCTT GGCGAGAAAG 180  
GCACCTTGCT GAAGGTTATG GAGAAGGCTT TTCCAGAACT AGGGTTAACT CAAAAGGATT 240  
GTACTGAAAT GAGCTGGATT GAAGCCGCCC TTTTCCATGG TGGRTTTCCT ACAGGKTCTC 300  
CTATTGAAAT TTTGCTTMAG CTCAAGTCGC CTYTAGGAAA AGRTTWCTTC AAAGCAACGK 360  
CGGATTCGT TAAAGAACCT WTTCTGTGA TAGGGCTCAA AGGAATATTC AAAAGATTGA 420

2  
cont.



## (2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 437 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Arabidopsis thaliana
  - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..437

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GTGTACTAT CATNGAAGAT TAAGTTAGTC GATGTTCCGT CCACGGTCAC CGNGTTTAAA 60  
GTCCAGAAAC ATNAGGAGAA AGAGGCCGTT AGGNTCATCA ACAAGTGGCA GTATGTTGCG 120  
GATAAGGTCC CTGAAGATCT TTTCATCAGC GCAACGTTGG NGAGATCAAA CGGAAACTCT 180  
GTGCAGGCTT TGTTTACTGG ACTCTATCTT GGNCCGGTGA ATAATNTCTT GGCCTTGATG 240  
GAAGAAAAGT TTCCAGANTT AGGTCTTGAT ATCCAAGNCT GCACAGAGAT GAGTTGGGCT 300  
GAATCTGCAC TCTGGTNTNC TGNTTTCNCT AAAGGAGAGN CTCCTTGGGT GTTCNCGCG 360  
GATCGGNAGC GGNCAATTTN TGGNCTTTCA AGGGGAAAGN CGGCTTTTTN CAAGAACCCG 420  
NTACCCGGGG TTCAATT 437

## (2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 441 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GCGGACCCTA TAGATCANNA TGTGCTACTG ANAGAAGAGG AAGCCAAGAA CAAGCCGGAG 60  
ACAGATAAAT ATCTGAAATG GGNCGATANC GTTTACGAAT TTATGACNCC ATATGTTTCG 120  
AAATCTCCAA GAGGAGCTTA TGTCAATTTT AAGGATATGG ATTTGGGTAT GTATCTTGGA 180  
AAGAAGAAGA CAAAGTACGA GGAAGGAAAG AGTTGGGGAG TGAAGTATTT CAAGAACAAT 240  
TTCGAGAGAT TGGTGAGAGT GAAGACTAGG GTTGATCCAA CAGATTTCTT CTGCGATGAA 300  
CAGAGCATTCTCTGGTGAA CAAAGTTACC TGAAGATATC ATTTGAAGTT TTTTATTAGT 360  
CCCTTTTCTC TGTGAAATCA TCTGTGCGTG TTGAATATTA TGCCTCAAGT GTGTAACCTA 420  
TGTGTGTGAT TGTGAATTGT G 441

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTGGCTTAAC ACAACGTCGT TTTGGGCCAA TTACCCGGCG GGTACACCCA AGAGCATCCT 60  
TCTAGATAGG CCTCCGACGA ATTCAGTGTC ATTTAAGAGT AAATCGGATT TTGTCAAAAA 120  
ACCAATACCC AAAAAAGGTT TAGAGAAGCT TTGGAAGACA ATGTTTAAAT TCAACAGTAG 180  
CGTCTCGTTG CAATTCAACC CTTACGGTGG AGTGATGGAC CGGATTCCGG CAACGGCCAC 240  
CGCTTTTCCT CATCGGAAAG GAAACTTGTT CAAGGTTCAA TACNCTACGA TGTGGTTTGA 300

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cont.

CGCAAACGCC ACACAGAGTA GCCNNGCTAT GATGAATGAG CTTTTTGAGG TGGCGGGACC 360  
 GTACGTGNGT CAAGTAAACC CGAGANANGG CTTCCTTTAA NTTTCAGAGNC CATCGNTNTT 420  
 NGGAGCAANN CCAAGTGGGG GGGNCCAACC GGGGGNTNAA ANCNAGNTC TTNGGGGGCC 480  
 CAGAATTTCC TTNGGGGAAT TT 502

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Arabidopsis thaliana
  - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 2..400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

NGGGAATTGC NCGAGGNAAG TTGTACCCAA TTCCTGGACC ACCATTGGTT TCCCAAGAAN 60  
 CCCGAGACAA CCGTTTTTCA ATNACCGTGA TGTGATTG GGTATTAATT CTCATAATGG 120  
 TAAAATCAGT AGTTATGTGG AAGGTAAACG TTACGGGAAG AAGTATTTTCG CAGGTAATTT 180  
 CGAGAGATTG GTGAAGATTA AGACGAGAGT TGATAGTGGT AATTTCTTTA GGAACGAACA 240  
 GAGTATTCCT GTGTTACCAT AAGTGATTTT ATTTGATTAT TGGTTAGTGA AATTTGTTGT 300  
 TGTATAATGA TTATATGTCG TATTTTATT TATTATTAGT AATTTATAAA GTTTGATATT 360  
 AAATACAAAT AGTATAATAA GATAGTTTCT TTAGTAAAA 400

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 383 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA

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Cont.

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CAACTCTAAT GGGAACACCT ACTTCGATCG AATGTCGATG GGGGAAGAGC TTTTCTGGGC 60  
GGTTCGAGGA GGTGGAGCCG CGAGTTTCGG CATCGTGATG GGATACAAA TCCGGTTGGT 120  
TCCGGTTCCG GAGAAAGTTA CGGTTTTTAG CGTCGGAAAA ACCGTCGGAG AAGGAGCCGT 180  
TGATCTTATA ATGAAGTGGC AGAACTTCTC TCATAGTACG GNTCGGAATT TTTTTGTGAA 240  
GCTGANTTTT GANTTTAGTC AACGGTGCAA AGCCGGGTGA AAAAAAGGTT TTAGNGNCTT 300  
TCANTTTGGN TGNAANCCTG GGGGTTTTAT NAGAACGGTT AACCAGGATT NANCCCGNGT 360  
TTCCCCGGGG TTAAACCTT NGG 383

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

ATCAATGTTT TACTAAACG TACACGAGCA TCGTTGGCTT TCAAGGCTAA ATCTGATTTT 60  
NTTCAAGAAC CGATNCCTAA AACCAGGATT TCGAAGCTTT GGAGACGGTT GCAAGAACCG 120  
GAAGCAGAGC ATGCTCAGCT AATTTNCACN CCATTTGGTG GTAAAATGAG TNAGATTGCA 180

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cont.

GATTACGAAA CACCATTTCC GCATAGGAAG GGAATATAT ATNAGATTCA GTACTTGAAT 240  
TACTGGAGAG GAGACGTGAA AGAGAAGTAT ATTGAGATNG GTGGAGGAGA GTTTACGGTT 300  
GNTATNAGTA AGTTTTTTGG CGAAGTNTNC CNAGAGGNGN CTTNNTNTAA ACCT 354

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 403 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Arabidopsis thaliana
  - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 2..403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TTTTTTAGTA CACTAATAAT CAAATGGAAT GAGAAATGAA GCCACAAAAG TATCTGCAAT 60  
CAAAATATCC TGCTATCTCC ATCTCAAGCT CTCAATAGTA TCCTCTCCGA AAGTGAAATC 120  
AACATTTCAA ACTCTATTTC TTGGTGGAAAT CGATAGACTG ATTCCTCTGA TGAACCAGAA 180  
GTTTCCGGAA CTCGGCTTAC GATCTCAAGA CTGTTCGGAA ATGAGCTGGA TCGAATCGAT 240  
AATGTTCTTC AACTGGAGAT CAGGACAGCC GTTAGAGATT TTGCTCAACA GAGACCTAAG 300  
GATTCGAGGA TCAGTATTTT AAAGCAAAGT CAGGATTATG GTTCAAAAAC CCGTTCCTGA 360  
AAACGTTTTT CGAAGAGGTA TCCAAGGGGT TTCTCGAGCA AGT 403

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 260 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO

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cont.

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```
GAGATGAGTT GGATTAANTC TGTACTCTGG TTTGCTGATT TCCCTAAAGG AGAATCTCTT 60
NGTGTTCTCA CGAATCGTAA GCGTACATCT CTATCTTTNA AAGGCAAAGA TGATTTTATC 120
CAAGAACCGA TACCCGAGGC TGCAATTNAA GAGATATGGA GGCGATTAGA AGCCCCCNAG 180
GCTCGGCTTG GAAAGATCAT ATTA ACTCCA TTTGGTGGGA AAATNAGTGA AATGGCAGAG 240
TACGTANCAC CATTCCCACA                                     260
```

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 605 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```
CTCTTG CATA TTCGCTG CAA GGATGGG AAA TTCAAAACCA CTCCCTACAA TTTTGTG TAT 60
TATAGTTTCA GTCTTGTATT TTTAATTCTA TTGCATAACA CCAACTTCTT CATCAGCCTC 120
CATCCAAGAT CAATTCATAA ACTGTGTCAA AAGAAACACA CATGTTTCTT TTCCACTCGA 180
GAAAACGTTA TTCACCCCTG CGAAAAACGT CTCTTTGTTC AACCAAGTCC TTGANTCGAC 240
GGCTCAAAAT CTCCAGTTCT TGGCAAAATC CATGCCTAAA CCGGGRTTCA TATTCAGACC 300
GATTCACCAG TCTCAAGTCC AAGSTTCCAT CATTTGTTCA AMGRAACTCG GGNTTCATTT 360
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Cont.

TNGTGTTTGA NGTGGCGGTC ACGATTTTCG AGGCCTTTGT NTTTATGTTT CACGGTTTGA 420  
 AAAAACCGTT TATATTACTC GGCCTGTCAA ANTTGNANNC AAAATCANAT GTTGGATATT 480  
 GNATTCCTAAA TAGGTNCTTG GGGTNAACCT GGTGGCTANC GTTTGGTGAG CTTTTACTTT 540  
 CAAGAATTTG CANGNGGANG TGCAAAGATT CCATGGGATT TCCCGGGGGG TTTNTTGCAC 600  
 AATGT 605

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 464 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Arabidopsis thaliana
  - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 2..464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

AACACAAAAC TCTTCCATTT GGCTTCTCTC TTGCATATTC GTTGCAAGGA TGGGAAATTC 60  
 AAAACCACTC CCTACAATTN CTTGTATTAT CGTTTCAGTC TTGTATTTTN NATTCTATTG 120  
 CATAACACCA ACTTCTTCAT CAGCCTCCAT CCAAGNTCAA TTCATAAACT GTGTCAAAAG 180  
 GAACACACAT GTTTCTTTTC CACTCGAGNA AACGGTATTC ACTCCTGCGG AAAACGGCTC 240  
 TTTTATTCAA CGGGTCNTG AATCGACGGG TCAAAATCTC CAGTTCTTGG NAAAATCCAT 300  
 GNCTAAACCG GGGTTCATAT TCAGGCCGGT TCACCAGTCT CAAGTCCAAG NTTCCATCAT 360  
 TTGTTCAAAG GAACTCGGGA TTCATTTCCG CGNTAGAAGT GGCGGGCANN GGTTCGGGG 420  
 CCTGTCTNTT GNTTANGGNN AGGAAAACCG GTTNTATTNC TCGG 464

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 386 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

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Cont

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

TCGGGAGCCC ANGNTAAATT ANNTGAAAAAT GGGGNCGNAT ANCCGTTTAC NGAATTTTAT 60  
GACNCCCAAT ATGTTTCGAA ATCTCAAAGA NNGGGANCTT ATGTCAATT CAAGGATATG 120  
GATTTGGGTA TGTATCTTGG AAAGNAGAAG ACAAAGTACG AGGAAGGAAA GAGTTGGGGA 180  
GTGAAGTATT TCAAGAACAA TTTCGAGAGA TTGGTGAGAG TGAAGACTAG GGTTGATCCN 240  
ACAGATTTTCN TCTGCGATGA ACAGAGCATT CCTCTGGTGN ACAAAGTTAC CTGAAGATAT 300  
CATTTGAAGT TTTTATTAG TCCCTTTTCT CTGTGAAATC ATCTGTGCGT GTTGAATANT 360  
ATGCGTCAAG TGTGTAACCT ATGTGT 386

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

TACCATAGGG AGGTGGTGNA AGATTTTGTA TGTAGNCTTA GGGGAAGGCG AGTAGTATGG 60

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Cont



TGGTGGTGGG GAGCTGTAAA CGTATGGTGG TGGTGGAGAT TTGTATGTGG GCTGGTTAAC 120  
TTCATTGAAG CTAAATCTG GGGACCTAAG TACTTCAAAG GCAATTTTGA CAGATTGGTG 180  
AAGATTAAAA CCAAGGTTGA TCCAGAGAAC TTCTTCAGGC ACGAGCAGAG TATCCACCT 240  
ATGCCCTACT AGAAGCTAGG TTCATGAAAC CAATAACATT ATCAAAAATA AGAATAAATG 300  
ATAATTGTAT ACAACATGAT TCGTCTTTCT TTATTTTCAGA CAATGTGGAC ACTACTCTAA 360  
ATAAAATGTC ATTTACC 377

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 377 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Arabidopsis thaliana
  - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..377
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

TACCATAGGG AGGTGGTGNA AGATTTTGTA TGTAGNCTTA GGGGAAGGCG AGTAGTATGG 60  
TGGTGGTGGG GAGCTGTAAA CGTATGGTGG TGGTGGAGAT TTGTATGTGG GCTGGTTAAC 120  
TTCATTGAAG CTAAATCTG GGGACCTAAG TACTTCAAAG GCAATTTTGA CAGATTGGTG 180  
AAGATTAAAA CCAAGGTTGA TCCAGAGAAC TTCTTCAGGC ACGAGCAGAG TATCCACCT 240  
ATGCCCTACT AGAAGCTAGG TTCATGAAAC CAATAACATT ATCAAAAATA AGAATAAATG 300  
ATAATTGTAT ACAACATGAT TCGTCTTTCT TTATTTTCAGA CAATGTGGAC ACTACTCTAA 360  
ATAAAATGTC ATTTACC 377

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 346 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

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cont

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GAGCTGTGGA TATGGTCACA AATGGCAATC GGTGGTCCG AAAACTGATC CGAATCTTTT 60  
TATGAGAATN TTGATTCAAC CAGTGACGAG GAAGAAGGTA AAGACTGTGA GAGCTTCTNT 120  
GGTTGCCCTN TTTTNAGGCN AGACAGATGA AGTTTTTGCT TTCCTTAGTA AGGAGTTTCC 180  
TGAATTGGGT TTAAAGAAGG AGAATTNTTC GGAGATGACT TGGTTTCANT CTGCTTTATG 240  
GTGGGACAAT CGTCTTAATG CTAATCAGGT TGATCCTAAA GTNTTCTTG ATCGGAATCT 300  
CGATACCTCG AGTTTCGGTA AGAGGAAATC GGATTACGTC GCGACT 346

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATGGGGTGAG ACTTATTTCA AAGGTAATTT CAAGAGATTA GGTGGGTTA AAGGGAAGNT 60  
TGATCCAACA AATTTCTTCA GGAACGAACA GAGTATTCCT CCTCTGTTTT GAGTCCTCAA 120

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Cont

TACAAAACCA GATATAAAG ATGTCATTTT ATTTTTTCAA TTATAATAGA TAATGTAAGT 180  
 TTCTGCTACA ATTGTAAAAG TGAGATGTAC CCAATACGGT TTAAGCGGAC CGAGAATAGT 240  
 CAATTCAAAG ACCAAATTCT G 261

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 478 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Arabidopsis thaliana
  - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GCTCAAAGGA CTAACCATGA AAACCTCCTC AAGTGTCTCT CTCACCGANT CAACGAGGAC 60  
 GACTCAAGAN TTATACACAC ATCAAAAGAT CCTTCGTATT TNTCAATCTT GATTTCTTCC 120  
 ATACAAAATC CAAGTTTCTC TGTTCTCGAA ACACCTAAAC CGGTTTCAAT CATCACTCCG 180  
 GTTCAAGCCA CCGATGTTCA ATCTACGNTT AAATNCGCAC GGNCTTCACG GGTATACACA 240  
 ATCAGGGCTA GGAGTGGTNG TCATGACTAC GGAGGTTTAT CTTTACATTG GCTTAAAAAN 300  
 CANNCCGTTT GTTNNTCATT GATTTNNAGA AATCTTCCGG GCTTATTTAA CATNTAAGAT 360  
 GTTTGATAAN CCGGNCCNG TTTGGGGTTC AAATCCCGGT GGCTTACAAA NTTNGGGGGA 420  
 ATGTGNCCTA TGAGGTTTGG AAAATTAANG CAAAATNTTT TGGGCCTTCC CGGCCGGT 478

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA

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Cont

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GGCCGTTAGG ATCATCAAGA AATGGCAATA TGCTGCAGAT AAGGTCCTG ATGATCTTTT 60  
CATTAGGACA ACATTGGAGA GATCAAACAA GAACGCAGTA CACGCTTTGT TCACTGGACT 120  
ATATATTGGT CCGGTGAACA ATCTATTGGC GTTGATGGAA GAAAAGTTTC CGGAAGTAGG 180  
TCTTGAGAAA GAAGGTTGTG AAGAGATGAG TTGGATTGAG TCTGTACTCT GGTTCGCTGA 240  
TTCCCTAAA GGAGAATCTC TTGGTGTCTT CACGAATCGT GAGCGTACAT CTCTATCTTT 300  
CAAAGGCAAA GATGATTTTG TCCAAGAACC GATACCCGAG GCTGCAATTC AAGAGATATG 360  
GAGGCGATTA GAAGCCCCCG AGGCTCGGCT TGGAAAAGATC ATATTAATCT CATTGGGGTG 420  
NGGNAAAATG AGTGAAATGG CAGAGNCCGA ACCACCAATT CCCACANNCG AGGGAGGGGA 480  
ACCCCTNTGN GGNTCAGAAT GTGGTTCCTG GNNNNNAAGN GGGNGCCAGN ACCAANCCGG 540  
GNCNGTAAAN CNTGNAATGG GCCNAACCCG TNCCGGATT 579

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Oryza sativa*

(B) STRAIN: Nipponbare, subsp. japonica

(D) DEVELOPMENTAL STAGE: etiolated shoot (8 days old)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..252

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Cont

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

TGTCCTGGAA GGTCCGCCTC GTGCAGGTTN CGACGACGGT GACGGTGTTT GTCGTCGGGA 60  
GGAACGTCGA CCAGGGCGCC GCNGACGTCG TCGCCAGATG GCAAGACGTC GCGCCGAGCC 120  
TCCCTCCCGA GCTCACCATA CGGGTGATCG TNCGAGGGCA GCGCGCCACG TTCCAGTCGC 180  
TGTACCTCGG CTCGTGCGCC GACCTGGTGC CGACGATGAG CAGCATGTTC CCGGAGCTCG 240  
GGATGACGAT TG 252

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactuca sativa
- (B) STRAIN: lollo bionda

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /label= Ambiguous  
/note= "Xaa = Cys or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 20..21
- (D) OTHER INFORMATION: /label= ambiguous  
/note= "Xaa-Xaa probably is Ser-Phe"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Thr Ser Thr Ser Ile Ile Asp Arg Phe Thr Gln Xaa Leu Asn Asn Arg  
1 5 10 15  
Ala Asp Pro Xaa Xaa  
20

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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Cont.

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Lactuca sativa  
(B) STRAIN: lollo bionda
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 1  
(D) OTHER INFORMATION: /label= ambiguous  
/note= "Xaa = probably Ser"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 3  
(D) OTHER INFORMATION: /label= unknown
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 5  
(D) OTHER INFORMATION: /label= ambiguous  
/note= "Xaa = probably Ser"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 12  
(D) OTHER INFORMATION: /label= ambiguous  
/note= "Xaa = probably Trp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 24  
(D) OTHER INFORMATION: /label= ambiguous  
/note= "Xaa = probably Tyr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

*al cont*

Xaa	Ile	Xaa	Val	Xaa	Ile	Glu	Asp	Glu	Thr	Ala	Xaa	Val	Gln	Ala	Gly
1			5						10					15	
Ala	Thr	Leu	Gly	Glu	Val	Tyr	Xaa								
			20												

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Lactuca sativa  
    (B) STRAIN: lollo bionda

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Ala Asp Pro Ser Phe Pro Leu Ser Gly Gln Leu Tyr Tyr Pro  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 32 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

ACTTCTACTT CTATTATTGA TAGGTTTACT CA

32

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 405 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Lactuca sativa  
    (B) STRAIN: lollo bionda

(ix) FEATURE:  
    (A) NAME/KEY: CDS  
    (B) LOCATION: 1..405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

ACT TCT ACT TCT ATT ATT GAT AGG TTT ACT CAA TGT CTA AAC AAC CGA 48  
Thr Ser Thr Ser Ile Ile Asp Arg Phe Thr Gln Cys Leu Asn Asn Arg  
1                    5                    10                    15

GCT GAC CCT TCT TTC CCG CTC AGT GGA CAA CTT TAC ACT CCC GAT AAC 96  
Ala Asp Pro Ser Phe Pro Leu Ser Gly Gln Leu Tyr Thr Pro Asp Asn  
20                    25                    30

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cont.

TCC	TCT	TTT	CCA	TCC	GTC	TTG	CAA	GCT	TAC	ATC	CGG	AAC	CTC	CGA	TTC	144
Ser	Ser	Phe	Pro	Ser	Val	Leu	Gln	Ala	Tyr	Ile	Arg	Asn	Leu	Arg	Phe	
		35						40					45			
AAT	GAA	TCC	ACG	ACT	CCC	AAA	CCC	ATC	TTA	ATC	ATC	ACC	GCC	TTA	CAC	192
Asn	Glu	Ser	Thr	Thr	Pro	Lys	Pro	Ile	Leu	Ile	Ile	Thr	Ala	Leu	His	
	50					55					60					
CCT	TCA	CAC	ATT	CAA	GCA	GCT	GTT	GTG	TGC	GCC	AAA	ACA	CAC	CGC	CTG	240
Pro	Ser	His	Ile	Gln	Ala	Ala	Val	Val	Cys	Ala	Lys	Thr	His	Arg	Leu	
	65				70					75					80	
CTA	ATG	AAA	ACC	AGA	AGC	GGA	GGC	CAT	GAT	TAT	GAG	GGG	CTT	TCC	TAT	288
Leu	Met	Lys	Thr	Arg	Ser	Gly	Gly	His	Asp	Tyr	Glu	Gly	Leu	Ser	Tyr	
				85					90					95		
GTG	ACC	AAT	TCG	AAC	CAA	CCC	TTT	TTT	GTT	GTT	GAC	ATG	TTC	AAC	TTA	336
Val	Thr	Asn	Ser	Asn	Gln	Pro	Phe	Phe	Val	Val	Asp	Met	Phe	Asn	Leu	
			100					105					110			
CGC	TCC	ATA	AAC	GTG	AGT	ATT	GAA	GAT	GAA	ACT	GCA	TGG	GTC	CAA	GCC	384
Arg	Ser	Ile	Asn	Val	Ser	Ile	Glu	Asp	Glu	Thr	Ala	Trp	Val	Gln	Ala	
		115					120					125				
GGC	GCC	ACC	CTC	GGA	GAA	GTT										405
Gly	Ala	Thr	Leu	Gly	Glu	Val										
	130					135										

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Thr Ser Thr Ser Ile Ile Asp Arg Phe Thr Gln Cys Leu Asn Asn Arg  
1 5 10 15

Ala Asp Pro Ser Phe Pro Leu Ser Gly Gln Leu Tyr Thr Pro Asp Asn  
20 25 30

Ser Ser Phe Pro Ser Val Leu Gln Ala Tyr Ile Arg Asn Leu Arg Phe  
35 40 45

Asn Glu Ser Thr Thr Pro Lys Pro Ile Leu Ile Ile Thr Ala Leu His  
50 55 60

Pro Ser His Ile Gln Ala Ala Val Val Cys Ala Lys Thr His Arg Leu  
65 70 75 80

Leu Met Lys Thr Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr  
85 90 95

al  
Cont



Val Thr Asn Ser Asn Gln Pro Phe Phe Val Val Asp Met Phe Asn Leu  
100 105 110

Arg Ser Ile Asn Val Ser Ile Glu Asp Glu Thr Ala Trp Val Gln Ala  
115 120 125

Gly Ala Thr Leu Gly Glu Val  
130 135

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CACGTTTATG GAGCGTAAGT TGAAC

25

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

CACCCTTCAC ACATTCAAGC AGC

23

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1981 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

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Cont.

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Lactuca sativa  
 (B) STRAIN: lollo bionda
- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 7..1626
- (ix) FEATURE:  
 (A) NAME/KEY: unsure  
 (B) LOCATION: replace(372, "g")
- (ix) FEATURE:  
 (A) NAME/KEY: unsure  
 (B) LOCATION: replace(379, "g")
- (ix) FEATURE:  
 (A) NAME/KEY: unsure  
 (B) LOCATION: replace(786, "t")
- (ix) FEATURE:  
 (A) NAME/KEY: unsure  
 (B) LOCATION: replace(1105..1106, "ga")  
 (D) OTHER INFORMATION: /note= "also possible "gg" and "aa"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ACAAAA ATG GCA ATT ACC TAT TCT TTC AAC TTC AAA TCT TAT ATT TTT 48  
 Met Ala Ile Thr Tyr Ser Phe Asn Phe Lys Ser Tyr Ile Phe  
 1 5 10

CCT CTC CTC CTT GTC TTG CTC TCT ACC CAT TCA TCA GCG ACT TCA ACT 96  
 Pro Leu Leu Leu Val Leu Leu Ser Thr His Ser Ser Ala Thr Ser Thr  
 15 20 25 30

TCC ATT ATA GAT CGC TTC ACC CAA TGT CTA AAC AAC CGA GCT GAC CCT 144  
 Ser Ile Ile Asp Arg Phe Thr Gln Cys Leu Asn Asn Arg Ala Asp Pro  
 35 40 45

TCT TTC CCG CTC AGT GGA CAA CTT TAC ACT CCC GAT AAC TCC TCT TTT 192  
 Ser Phe Pro Leu Ser Gly Gln Leu Tyr Thr Pro Asp Asn Ser Ser Phe  
 50 55 60

CCA TCC GTC TTG CAA GCT TAC ATC CGG AAC CTC CGA TTC AAT GAA TCC 240  
 Pro Ser Val Leu Gln Ala Tyr Ile Arg Asn Leu Arg Phe Asn Glu Ser  
 65 70 75

ACG ACT CCC AAA CCC ATC TTA ATC ATC ACC GCC TTA CAC CCT TCA CAC 288  
 Thr Thr Pro Lys Pro Ile Leu Ile Ile Thr Ala Leu His Pro Ser His  
 80 85 90

ATT CAA GCA GCT GTT GTG TGC GCC AAA ACA CAC CGC CTG CTA ATG AAA 336  
 Ile Gln Ala Ala Val Val Cys Ala Lys Thr His Arg Leu Leu Met Lys  
 95 100 105 110

ACC AGA AGC GGA GGC CAT GAT TAT GAG GGG CTT TCC TAT GTG ACC AAT 384  
 Thr Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Val Thr Asn  
 115 120 125

at  
cont.

TCG AAC CAA CCC TTT TTT GTT GTT GAC ATG TTC AAC TTA CGC TCC ATA	432
Ser Asn Gln Pro Phe Phe Val Val Asp Met Phe Asn Leu Arg Ser Ile	
130 135 140	
AAC GTG AGT ATT GAA GAT GAA ACT GCA TGG GTC CAA GCT GGT GCG ACT	480
Asn Val Ser Ile Glu Asp Glu Thr Ala Trp Val Gln Ala Gly Ala Thr	
145 150 155	
CTT GGT GAA GTC TAC TAC CGA ATA GCA GAG AAA AGC AAC AGT CAT GCT	528
Leu Gly Glu Val Tyr Tyr Arg Ile Ala Glu Lys Ser Asn Ser His Ala	
160 165 170	
TTT CCG GCT GGC GTT TGC CCT ACT GTT GGA GTT GGT GGC CAT TTT AGT	576
Phe Pro Ala Gly Val Cys Pro Thr Val Gly Val Gly Gly His Phe Ser	
175 180 185 190	
GGT GGT GGT TAT GGT AAC TTG ATG GGA AAA TAC GGC CTT TCT GTT GAC	624
Gly Gly Gly Tyr Gly Asn Leu Met Gly Lys Tyr Gly Leu Ser Val Asp	
195 200 205	
AAT ATT GTC GAT GCT CAG TTA ATC GAT GTG AAT GGT AAA CTT CTG AAT	672
Asn Ile Val Asp Ala Gln Leu Ile Asp Val Asn Gly Lys Leu Leu Asn	
210 215 220	
CGG AAA TCA ATG GGT GAA GAT CTT TTT TGG GCC ATC ACA GGT GGT GGT	720
Arg Lys Ser Met Gly Glu Asp Leu Phe Trp Ala Ile Thr Gly Gly Gly	
225 230 235	
GGT GTC AGC TTT GGT GTG GTT GTA GCG TAC AAG ATC AAA CTG GTT CGT	768
Gly Val Ser Phe Gly Val Val Val Ala Tyr Lys Ile Lys Leu Val Arg	
240 245 250	
GTT CCT ACC ACT GTG ACC GTT TTT AAC GTA CAA AGA ACA TCC GAG CAG	816
Val Pro Thr Thr Val Thr Val Phe Asn Val Gln Arg Thr Ser Glu Gln	
255 260 265 270	
AAC CTA AGC ACC ATA GCC CAC CGA TGG ATA CAA GTT GCG GAT AAG CTC	864
Asn Leu Ser Thr Ile Ala His Arg Trp Ile Gln Val Ala Asp Lys Leu	
275 280 285	
GAT AAT GAC CTT TTC CTT CGA ATG ACC TTT AAC GTG ATA AAC AAC ACA	912
Asp Asn Asp Leu Phe Leu Arg Met Thr Phe Asn Val Ile Asn Asn Thr	
290 295 300	
AAT GGC GAA AAG ACG ATA CGT GGT TTG TTT CCA ACA CTG TAC CTC GGA	960
Asn Gly Glu Lys Thr Ile Arg Gly Leu Phe Pro Thr Leu Tyr Leu Gly	
305 310 315	
AAC TCT ACC GCT CTT GTT GCC CTC CTG AAC AAG GAT TTC CCT GAA TTA	1008
Asn Ser Thr Ala Leu Val Ala Leu Leu Asn Lys Asp Phe Pro Glu Leu	
320 325 330	
GGT GTA GAA ATT TCA GAT TGT ATT GAA ATG AGT TGG ATC GAG TCT GTT	1056
Gly Val Glu Ile Ser Asp Cys Ile Glu Met Ser Trp Ile Glu Ser Val	
335 340 345 350	

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Cont.

CTT TTC TAC ACA AAC TTC CCC ATT GGT ACT CCG ACC ACT GCT CTT CTA 1104  
Leu Phe Tyr Thr Asn Phe Pro Ile Gly Thr Pro Thr Thr Ala Leu Leu  
355 360 365

AGC CGT ACA CCT CAA AGA CTA AAC CCA TTC AAA ATC AAA TCT GAT TAC 1152  
Ser Arg Thr Pro Gln Arg Leu Asn Pro Phe Lys Ile Lys Ser Asp Tyr  
370 375 380

GTA AAA AAC ACT ATT TCC AAA CAG GGA TTC GAA TCC ATA TTT GAA AGG 1200  
Val Lys Asn Thr Ile Ser Lys Gln Gly Phe Glu Ser Ile Phe Glu Arg  
385 390 395

ATG AAA GAA CTC GAA AAC CAA ATG CTA GCT TTC AAC CCT TAT GGT GGA 1248  
Met Lys Glu Leu Glu Asn Gln Met Leu Ala Phe Asn Pro Tyr Gly Gly  
400 405 410

AGA ATG AGC GAA ATT TCC GAA TTT GCA AAG CCT TTT CCC CAT CGA TCA 1296  
Arg Met Ser Glu Ile Ser Glu Phe Ala Lys Pro Phe Pro His Arg Ser  
415 420 425 430

GGG AAT ATA GCG AAG ATC CAA TAC GAA GTA AAC TGG GAT GAA CTT GGC 1344  
Gly Asn Ile Ala Lys Ile Gln Tyr Glu Val Asn Trp Asp Glu Leu Gly  
435 440 445

GTT GAA GCA GCC AAT CGG TAC TTG AAC TTC ACA AGG GTG ATG TAT GAT 1392  
Val Glu Ala Ala Asn Arg Tyr Leu Asn Phe Thr Arg Val Met Tyr Asp  
450 455 460

TAT ATG ACT CCG TTT GTT TCT AAG AAC CCC AGG GAA GCA TTT CTG AAC 1440  
Tyr Met Thr Pro Phe Val Ser Lys Asn Pro Arg Glu Ala Phe Leu Asn  
465 470 475

TAC AGG GAT TTA GAT ATT GGT GTC AAC AGT CAT GGC AAG AAT GCT TAC 1488  
Tyr Arg Asp Leu Asp Ile Gly Val Asn Ser His Gly Lys Asn Ala Tyr  
480 485 490

GGT GAA GGA ATG GTT TAT GGG CAC AAG TAT TTC AAA GAG ACG AAT TAT 1536  
Gly Glu Gly Met Val Tyr Gly His Lys Tyr Phe Lys Glu Thr Asn Tyr  
495 500 505 510

AAG AGG CTA ACG ATG GTG AAG ACG AGG GTT GAT CCT AGC AAT TTT TTT 1584  
Lys Arg Leu Thr Met Val Lys Thr Arg Val Asp Pro Ser Asn Phe Phe  
515 520 525

AGG AAT GAG CAA AGT ATC CCA ACT TTG TCA TCT TCA TGG AAG 1626  
Arg Asn Glu Gln Ser Ile Pro Thr Leu Ser Ser Ser Trp Lys  
530 535 540

TAAATTCTAA ATTCACTTGT GAAATTGAAT AAAAGTATGG CTTTTTCAAG GTCATGGTAT 1686

CCAGATTCAG ATGATATTGA TATAATTTTG ACTTGTATTT ATACAAACAA AATTATATTA 1746

TATTTTTCTG AATTTAGATT TTCCATTCTT TGGAAAAATA TACGAACATT GATGTTGATA 1806

TTTTTAAGAA TTATAGATTT TGAACATTGT GAACAATGAA TAAACCGAGG ACTTCCCTTG 1866

GGTTTTTTTTT ATAAGTATGT AATAGCATGT CTTTAATCAA GATAACCGAT CATTGGATGC 1926

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## (2) INFORMATION FOR SEQ ID NO: 58:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Met Ala Ile Thr Tyr Ser Phe Asn Phe Lys Ser Tyr Ile Phe Pro Leu  
 1 5 10 15  
 Leu Leu Val Leu Leu Ser Thr His Ser Ser Ala Thr Ser Thr Ser Ile  
 20 25 30  
 Ile Asp Arg Phe Thr Gln Cys Leu Asn Asn Arg Ala Asp Pro Ser Phe  
 35 40 45  
 Pro Leu Ser Gly Gln Leu Tyr Thr Pro Asp Asn Ser Ser Phe Pro Ser  
 50 55 60  
 Val Leu Gln Ala Tyr Ile Arg Asn Leu Arg Phe Asn Glu Ser Thr Thr  
 65 70 75 80  
 Pro Lys Pro Ile Leu Ile Ile Thr Ala Leu His Pro Ser His Ile Gln  
 85 90 95  
 Ala Ala Val Val Cys Ala Lys Thr His Arg Leu Leu Met Lys Thr Arg  
 100 105 110  
 Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Val Thr Asn Ser Asn  
 115 120 125  
 Gln Pro Phe Phe Val Val Asp Met Phe Asn Leu Arg Ser Ile Asn Val  
 130 135 140  
 Ser Ile Glu Asp Glu Thr Ala Trp Val Gln Ala Gly Ala Thr Leu Gly  
 145 150 155 160  
 Glu Val Tyr Tyr Arg Ile Ala Glu Lys Ser Asn Ser His Ala Phe Pro  
 165 170 175  
 Ala Gly Val Cys Pro Thr Val Gly Val Gly Gly His Phe Ser Gly Gly  
 180 185 190  
 Gly Tyr Gly Asn Leu Met Gly Lys Tyr Gly Leu Ser Val Asp Asn Ile  
 195 200 205  
 Val Asp Ala Gln Leu Ile Asp Val Asn Gly Lys Leu Leu Asn Arg Lys  
 210 215 220  
 Ser Met Gly Glu Asp Leu Phe Trp Ala Ile Thr Gly Gly Gly Gly Val  
 225 230 235 240

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 Cnt

Ser Phe Gly Val Val Val Ala Tyr Lys Ile Lys Leu Val Arg Val Pro  
 245 250 255  
 Thr Thr Val Thr Val Phe Asn Val Gln Arg Thr Ser Glu Gln Asn Leu  
 260 265 270  
 Ser Thr Ile Ala His Arg Trp Ile Gln Val Ala Asp Lys Leu Asp Asn  
 275 280 285  
 Asp Leu Phe Leu Arg Met Thr Phe Asn Val Ile Asn Asn Thr Asn Gly  
 290 295 300  
 Glu Lys Thr Ile Arg Gly Leu Phe Pro Thr Leu Tyr Leu Gly Asn Ser  
 305 310 315 320  
 Thr Ala Leu Val Ala Leu Leu Asn Lys Asp Phe Pro Glu Leu Gly Val  
 325 330 335  
 Glu Ile Ser Asp Cys Ile Glu Met Ser Trp Ile Glu Ser Val Leu Phe  
 340 345 350  
 Tyr Thr Asn Phe Pro Ile Gly Thr Pro Thr Thr Ala Leu Leu Ser Arg  
 355 360 365  
 Thr Pro Gln Arg Leu Asn Pro Phe Lys Ile Lys Ser Asp Tyr Val Lys  
 370 375 380  
 Asn Thr Ile Ser Lys Gln Gly Phe Glu Ser Ile Phe Glu Arg Met Lys  
 385 390 395 400  
 Glu Leu Glu Asn Gln Met Leu Ala Phe Asn Pro Tyr Gly Gly Arg Met  
 405 410 415  
 Ser Glu Ile Ser Glu Phe Ala Lys Pro Phe Pro His Arg Ser Gly Asn  
 420 425 430  
 Ile Ala Lys Ile Gln Tyr Glu Val Asn Trp Asp Glu Leu Gly Val Glu  
 435 440 445  
 Ala Ala Asn Arg Tyr Leu Asn Phe Thr Arg Val Met Tyr Asp Tyr Met  
 450 455 460  
 Thr Pro Phe Val Ser Lys Asn Pro Arg Glu Ala Phe Leu Asn Tyr Arg  
 465 470 475 480  
 Asp Leu Asp Ile Gly Val Asn Ser His Gly Lys Asn Ala Tyr Gly Glu  
 485 490 495  
 Gly Met Val Tyr Gly His Lys Tyr Phe Lys Glu Thr Asn Tyr Lys Arg  
 500 505 510  
 Leu Thr Met Val Lys Thr Arg Val Asp Pro Ser Asn Phe Phe Arg Asn  
 515 520 525  
 Glu Gln Ser Ile Pro Thr Leu Ser Ser Ser Trp Lys  
 530 535 540

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 Cont.

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GGTAATGATC TCCTTTCTTG TTTGACC

27

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

AGAGCGGCCG CTATATTACA ACTTCTCCAC CATCACTCCT C

41

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GGTGATGTTA ATGATAATCT CCTC

24

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid

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cont.

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

AGAGCGGCCG CTACAATTCC TTCAACATGT AAATTTCTC

40

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ACTTCCCGTA GAAACTCGGA GACTTTCACA CAATGC

36

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

TCCATCCAAG ATCAATTCAT AAAGTGTGTC

30

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

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cont.



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

AGAGCGGCCG CTTTCATGAA CCTAGCTTCT AGTAGG

36

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

AGAGCGGCCG CGAAATGGCC CCCCTTTTAA AACGGGG

37

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

AGAGCGGCCG CAAATGATAT CTTCAGGTAA CTTGTTCAC

40

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

AGAGCGGCCG CATAATCAAA TAAATACACT TATGGTAACA CAG

43

(2) INFORMATION FOR SEQ ID NO: 69:

a!  
Cont.

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 38 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

AGAGCGGCCG CTGGTTTTGT ATTGAGGACT CAAAACAG

38

(2) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1757 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana  
 (B) STRAIN: Colombia

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: join(1..570, 801..1754)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

ACT TCC CGT AGA AAC TCG GAG ACT TTC ACA CAA TGC CTA ACC TCA AAC 48  
 Thr Ser Arg Arg Asn Ser Glu Thr Phe Thr Gln Cys Leu Thr Ser Asn  
 1 5 10 15

TCC GAC CCC AAA CAT CCC ATC TCC CCC GCT ATC TTC TTC TCC GGA AAT 96  
 Ser Asp Pro Lys His Pro Ile Ser Pro Ala Ile Phe Phe Ser Gly Asn  
 20 25 30

GGC TCC TAC TCC TCC GTA TTA CAA GCC AAC ATC CGT AAC CTC CGC TTC 144  
 Gly Ser Tyr Ser Ser Val Leu Gln Ala Asn Ile Arg Asn Leu Arg Phe  
 35 40 45

AAC ACC ACC TCA ACT CCG AAA CCC TTC CTC ATA ATC GCC GCA ACA CAT 192  
 Asn Thr Thr Ser Thr Pro Lys Pro Phe Leu Ile Ile Ala Ala Thr His  
 50 55 60

GAA TCC CAT GTG CAA GCC GCG ATT ACT TGC GGG AAA CGC CAC AAC CTT 240  
 Glu Ser His Val Gln Ala Ala Ile Thr Cys Gly Lys Arg His Asn Leu  
 65 70 75 80

al  
cont.

CAG ATG AAA ATC AGA AGT GGA GGC CAC GAC TAC GAT GGC TTG TCA TAC	288
Gln Met Lys Ile Arg Ser Gly Gly His Asp Tyr Asp Gly Leu Ser Tyr	
85 90 95	
GTT ACA TAC TCT GGC AAA CCG TTC TTC GTC CTC GAC ATG TTT AAC CTC	336
Val Thr Tyr Ser Gly Lys Pro Phe Phe Val Leu Asp Met Phe Asn Leu	
100 105 110	
CGT TCG GTG GAT GTC GAT GTG GCA AGT AAG ACC GCG TGG GTC CAA ACC	384
Arg Ser Val Asp Val Asp Val Ala Ser Lys Thr Ala Trp Val Gln Thr	
115 120 125	
GGT GCC ATA CTC GGA GAA GTT TAT TAC TAT ATA TGG GAG AAG AGC AAA	432
Gly Ala Ile Leu Gly Glu Val Tyr Tyr Tyr Ile Trp Glu Lys Ser Lys	
130 135 140	
ACC CTA GCT TAT CCC GCC GGA ATT TGT CCC ACG GTT GGT GTC GGT GGC	480
Thr Leu Ala Tyr Pro Ala Gly Ile Cys Pro Thr Val Gly Val Gly Gly	
145 150 155 160	
CAT ATC AGT GGT GGA GGT TAC GGT AAC ATG ATG AGA AAA TAC GGT CTC	528
His Ile Ser Gly Gly Gly Tyr Gly Asn Met Met Arg Lys Tyr Gly Leu	
165 170 175	
ACC GTA GAT AAT ACC ATC GAT GCA AGA ATG GTC GAC GTT AAT	570
Thr Val Asp Asn Thr Ile Asp Ala Arg Met Val Asp Val Asn	
180 185 190	
GGTATAATTG ATATCTCTAT TTTATATACT AATTAAATTT TATAGTGTGG ATCGGATAGT	630
GATTTTGGTC CATCAATTAA AAAGTTGGTG AACATAAAAT TAACCAAGCA ATCAATTTAG	690
ACAAGCAACA TAATCATATA TATTTTTCTT ACATTTGTAT GTACCTGAAT ATTTATATTT	750
ATGTTTATAT GTTCTCACTA TATTTTCACT TTTGTATTTG AAAATTTTTA GGA AAA	806
Gly Lys	
ATT TTG GAT AGA AAA TTG ATG GGA GAA GAT CTC TAC TGG GCA ATA AAC	854
Ile Leu Asp Arg Lys Leu Met Gly Glu Asp Leu Tyr Trp Ala Ile Asn	
195 200 205	
GGA GGA GGA GGA GGG AGC TAC GGC GTC GTA TTG GCC TAC AAA ATA AAC	902
Gly Gly Gly Gly Gly Ser Tyr Gly Val Val Leu Ala Tyr Lys Ile Asn	
210 215 220	
CTT GTT GAA GTC CCA GAA AAC GTC ACC GTT TTC AGA ATC TCC CGG ACG	950
Leu Val Glu Val Pro Glu Asn Val Thr Val Phe Arg Ile Ser Arg Thr	
225 230 235 240	
TTA GAA CAA AAT GCG ACG GAT ATC ATT CAC CGG TGG CAA CAA GTT GCA	998
Leu Glu Gln Asn Ala Thr Asp Ile Ile His Arg Trp Gln Gln Val Ala	
245 250 255	
CCG AAG CTT CCC GAC GAG CTT TTC ATA AGA ACA GTC ATT GAC GTA GTA	1046
Pro Lys Leu Pro Asp Glu Leu Phe Ile Arg Thr Val Ile Asp Val Val	
260 265 270	

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cont.

AAC	GGC	ACT	GTT	TCA	TCT	CAA	AAG	ACC	GTC	AGG	ACA	ACA	TTC	ATA	GCA	1094
Asn	Gly	Thr	Val	Ser	Ser	Gln	Lys	Thr	Val	Arg	Thr	Thr	Phe	Ile	Ala	
		275					280						285			
ATG	TTT	CTA	GGA	GAC	ACG	ACA	ACT	CTA	CTG	TCG	ATA	TTA	AAC	CGG	AGA	1142
Met	Phe	Leu	Gly	Asp	Thr	Thr	Thr	Leu	Leu	Ser	Ile	Leu	Asn	Arg	Arg	
	290						295				300					
TTC	CCA	GAA	TTG	GGT	TTG	GTC	CGG	TCT	GAC	TGT	ACC	GAA	ACA	AGC	TGG	1190
Phe	Pro	Glu	Leu	Gly	Leu	Val	Arg	Ser	Asp	Cys	Thr	Glu	Thr	Ser	Trp	
305					310					315					320	
ATC	CAA	TCT	GTG	CTA	TTC	TGG	ACA	AAT	ATC	CAA	GTT	GGT	TCG	TCG	GAG	1238
Ile	Gln	Ser	Val	Leu	Phe	Trp	Thr	Asn	Ile	Gln	Val	Gly	Ser	Ser	Glu	
			325						330					335		
ACA	CTT	CTA	CTC	CAA	AGG	AAT	CAA	CCC	GTG	AAC	TAC	CTC	AAG	AGG	AAA	1286
Thr	Leu	Leu	Leu	Gln	Arg	Asn	Gln	Pro	Val	Asn	Tyr	Leu	Lys	Arg	Lys	
		340						345					350			
TCA	GAT	TAC	GTA	CGT	GAA	CCG	ATT	TCA	AGA	ACC	GGT	TTA	GAG	TCA	ATT	1334
Ser	Asp	Tyr	Val	Arg	Glu	Pro	Ile	Ser	Arg	Thr	Gly	Leu	Glu	Ser	Ile	
	355						360					365				
TGG	AAG	AAA	ATG	ATC	GAG	CTT	GAA	ATT	CCG	ACA	ATG	GCT	TTC	AAT	CCA	1382
Trp	Lys	Lys	Met	Ile	Glu	Leu	Glu	Ile	Pro	Thr	Met	Ala	Phe	Asn	Pro	
	370					375					380					
TAC	GGT	GGT	GAG	ATG	GGG	AGG	ATA	TCA	TTA	CGG	GTG	ACT	CCG	TTC	CCA	1430
Tyr	Gly	Gly	Glu	Met	Gly	Arg	Ile	Ser	Leu	Arg	Val	Thr	Pro	Phe	Pro	
385					390					395					400	
TAC	AGA	GCC	GGT	AAT	CTC	TGG	AAG	ATT	CAG	TAC	GGT	GCG	AAT	TGG	AGA	1478
Tyr	Arg	Ala	Gly	Asn	Leu	Trp	Lys	Ile	Gln	Tyr	Gly	Ala	Asn	Trp	Arg	
			405						410					415		
GAT	GAG	ACT	TTA	ACC	GAC	CGG	TAC	ATG	GAA	TTG	ACG	AGG	AAG	TTG	TAC	1526
Asp	Glu	Thr	Leu	Thr	Asp	Arg	Tyr	Met	Glu	Leu	Thr	Arg	Lys	Leu	Tyr	
		420						425					430			
CAA	TTC	ATG	ACA	CCA	TTT	GTT	TCC	AAG	AAT	CCG	AGA	CAA	TCG	TTT	TTC	1574
Gln	Phe	Met	Thr	Pro	Phe	Val	Ser	Lys	Asn	Pro	Arg	Gln	Ser	Phe	Phe	
		435						440					445			
AAT	AAC	CGT	GAT	GTT	GAT	TTG	GGT	ATT	AAT	TCT	CAT	AAT	GGT	AAA	ATC	1622
Asn	Asn	Arg	Asp	Val	Asp	Leu	Gly	Ile	Asn	Ser	His	Asn	Gly	Lys	Ile	
	450						455				460					
AGT	AGT	TAT	GTG	GAA	GGT	AAA	CGT	TAC	GGG	AAG	AAG	TAT	TTC	GCA	GGT	1670
Ser	Ser	Tyr	Val	Glu	Gly	Lys	Arg	Tyr	Gly	Lys	Lys	Tyr	Phe	Ala	Gly	
465					470					475					480	
AAT	TTC	GAG	AGA	TTG	GTG	AAG	ATT	AAG	ACG	AGA	GTT	GAT	AGT	GGT	AAT	1718
Asn	Phe	Glu	Arg	Leu	Val	Lys	Ile	Lys	Thr	Arg	Val	Asp	Ser	Gly	Asn	
				485					490					495		

a!  
cont.

TTC TTT AGG AAC GAA CAC AGT ATT CCT GTG TTA CCA TAA  
Phe Phe Arg Asn Glu His Ser Ile Pro Val Leu Pro  
500 505

1757

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

Thr	Ser	Arg	Arg	Asn	Ser	Glu	Thr	Phe	Thr	Gln	Cys	Leu	Thr	Ser	Asn	1	5	10	15
Ser	Asp	Pro	Lys	His	Pro	Ile	Ser	Pro	Ala	Ile	Phe	Phe	Ser	Gly	Asn	20	25	30	
Gly	Ser	Tyr	Ser	Ser	Val	Leu	Gln	Ala	Asn	Ile	Arg	Asn	Leu	Arg	Phe	35	40	45	
Asn	Thr	Thr	Ser	Thr	Pro	Lys	Pro	Phe	Leu	Ile	Ile	Ala	Ala	Thr	His	50	55	60	
Glu	Ser	His	Val	Gln	Ala	Ala	Ile	Thr	Cys	Gly	Lys	Arg	His	Asn	Leu	65	70	75	80
Gln	Met	Lys	Ile	Arg	Ser	Gly	Gly	His	Asp	Tyr	Asp	Gly	Leu	Ser	Tyr	85	90	95	
Val	Thr	Tyr	Ser	Gly	Lys	Pro	Phe	Phe	Val	Leu	Asp	Met	Phe	Asn	Leu	100	105	110	
Arg	Ser	Val	Asp	Val	Asp	Val	Ala	Ser	Lys	Thr	Ala	Trp	Val	Gln	Thr	115	120	125	
Gly	Ala	Ile	Leu	Gly	Glu	Val	Tyr	Tyr	Tyr	Ile	Trp	Glu	Lys	Ser	Lys	130	135	140	
Thr	Leu	Ala	Tyr	Pro	Ala	Gly	Ile	Cys	Pro	Thr	Val	Gly	Val	Gly	Gly	145	150	155	160
His	Ile	Ser	Gly	Gly	Gly	Tyr	Gly	Asn	Met	Met	Arg	Lys	Tyr	Gly	Leu	165	170	175	
Thr	Val	Asp	Asn	Thr	Ile	Asp	Ala	Arg	Met	Val	Asp	Val	Asn	Gly	Lys	180	185	190	
Ile	Leu	Asp	Arg	Lys	Leu	Met	Gly	Glu	Asp	Leu	Tyr	Trp	Ala	Ile	Asn	195	200	205	
Gly	Gly	Gly	Gly	Gly	Ser	Tyr	Gly	Val	Val	Leu	Ala	Tyr	Lys	Ile	Asn	210	215	220	

at  
Cont

Leu Val Glu Val Pro Glu Asn Val Thr Val Phe Arg Ile Ser Arg Thr  
 225 230 235 240  
 Leu Glu Gln Asn Ala Thr Asp Ile Ile His Arg Trp Gln Gln Val Ala  
 245 250 255  
 Pro Lys Leu Pro Asp Glu Leu Phe Ile Arg Thr Val Ile Asp Val Val  
 260 265 270  
 Asn Gly Thr Val Ser Ser Gln Lys Thr Val Arg Thr Thr Phe Ile Ala  
 275 280 285  
 Met Phe Leu Gly Asp Thr Thr Thr Leu Leu Ser Ile Leu Asn Arg Arg  
 290 295 300  
 Phe Pro Glu Leu Gly Leu Val Arg Ser Asp Cys Thr Glu Thr Ser Trp  
 305 310 315 320  
 Ile Gln Ser Val Leu Phe Trp Thr Asn Ile Gln Val Gly Ser Ser Glu  
 325 330 335  
 Thr Leu Leu Leu Gln Arg Asn Gln Pro Val Asn Tyr Leu Lys Arg Lys  
 340 345 350  
 Ser Asp Tyr Val Arg Glu Pro Ile Ser Arg Thr Gly Leu Glu Ser Ile  
 355 360 365  
 Trp Lys Lys Met Ile Glu Leu Glu Ile Pro Thr Met Ala Phe Asn Pro  
 370 375 380  
 Tyr Gly Gly Glu Met Gly Arg Ile Ser Leu Arg Val Thr Pro Phe Pro  
 385 390 395 400  
 Tyr Arg Ala Gly Asn Leu Trp Lys Ile Gln Tyr Gly Ala Asn Trp Arg  
 405 410 415  
 Asp Glu Thr Leu Thr Asp Arg Tyr Met Glu Leu Thr Arg Lys Leu Tyr  
 420 425 430  
 Gln Phe Met Thr Pro Phe Val Ser Lys Asn Pro Arg Gln Ser Phe Phe  
 435 440 445  
 Asn Asn Arg Asp Val Asp Leu Gly Ile Asn Ser His Asn Gly Lys Ile  
 450 455 460  
 Ser Ser Tyr Val Glu Gly Lys Arg Tyr Gly Lys Lys Tyr Phe Ala Gly  
 465 470 475 480  
 Asn Phe Glu Arg Leu Val Lys Ile Lys Thr Arg Val Asp Ser Gly Asn  
 485 490 495  
 Phe Phe Arg Asn Glu His Ser Ile Pro Val Leu Pro  
 500 505

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

*a!*  
*Cont*

(A) LENGTH: 1527 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana  
 (B) STRAIN: Colombia

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 1..1524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

ACT	TCC	CGT	AGA	AAC	TCG	GAG	ACT	TTC	ACA	CAA	TGC	CTA	ACC	TCA	AAC	48
Thr	Ser	Arg	Arg	Asn	Ser	Glu	Thr	Phe	Thr	Gln	Cys	Leu	Thr	Ser	Asn	
1				5				10						15		
TCC	GAC	CCC	AAA	CAT	CCC	ATC	TCC	CCC	GCT	ATC	TTC	TTC	TCC	GGA	AAT	96
Ser	Asp	Pro	Lys	His	Pro	Ile	Ser	Pro	Ala	Ile	Phe	Phe	Ser	Gly	Asn	
			20					25						30		
GGC	TCC	TAC	TCC	TCC	GTA	TTA	CAA	GCC	AAC	ATC	CGT	AAC	CTC	CGC	TTC	144
Gly	Ser	Tyr	Ser	Ser	Val	Leu	Gln	Ala	Asn	Ile	Arg	Asn	Leu	Arg	Phe	
		35					40						45			
AAC	ACC	ACC	TCA	ACT	CCG	AAA	CCC	TTC	CTC	ATA	ATC	GCC	GCA	ACA	CAT	192
Asn	Thr	Thr	Ser	Thr	Pro	Lys	Pro	Phe	Leu	Ile	Ile	Ala	Ala	Thr	His	
		50				55						60				
GAA	TCC	CAT	GTG	CAA	GCC	GCG	ATT	ACT	TGC	GGG	AAA	CGC	CAC	AAC	CTT	240
Glu	Ser	His	Val	Gln	Ala	Ala	Ile	Thr	Cys	Gly	Lys	Arg	His	Asn	Leu	
65				70						75				80		
CAG	ATG	AAA	ATC	AGA	AGT	GGA	GGC	CAC	GAC	TAC	GAT	GGC	TTG	TCA	TAC	288
Gln	Met	Lys	Ile	Arg	Ser	Gly	Gly	His	Asp	Tyr	Asp	Gly	Leu	Ser	Tyr	
				85					90					95		
GTT	ACA	TAC	TCT	GGC	AAA	CCG	TTC	TTC	GTC	CTC	GAC	ATG	TTT	AAC	CTC	336
Val	Thr	Tyr	Ser	Gly	Lys	Pro	Phe	Phe	Val	Leu	Asp	Met	Phe	Asn	Leu	
			100					105						110		
CGT	TCG	GTG	GAT	GTC	GAC	GTG	GCA	AGT	AAG	ACC	GCG	TGG	GTC	CAA	ACC	384
Arg	Ser	Val	Asp	Val	Asp	Val	Ala	Ser	Lys	Thr	Ala	Trp	Val	Gln	Thr	
		115					120					125				
GGT	GCC	ATA	CTC	GGA	GAA	GTT	TAT	TAC	TAT	ATA	TGG	GAG	AAG	AGC	AAA	432
Gly	Ala	Ile	Leu	Gly	Glu	Val	Tyr	Tyr	Tyr	Ile	Trp	Glu	Lys	Ser	Lys	
	130					135					140					
ACC	CTA	GCT	TAT	CCC	GCC	GGA	ATT	TGT	CCC	ACG	GTT	GGT	GTC	GGT	GGC	480

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cont.

Thr	Leu	Ala	Tyr	Pro	Ala	Gly	Ile	Cys	Pro	Thr	Val	Gly	Val	Gly	Gly	
145					150					155					160	
CAT	ATC	AGT	GGT	GGA	GGT	TAC	GGT	AAC	ATG	ATG	AGA	AAA	TAC	GGT	CTC	528
His	Ile	Ser	Gly	Gly	Gly	Tyr	Gly	Asn	Met	Met	Arg	Lys	Tyr	Gly	Leu	
			165					170						175		
ACC	GTA	GAT	AAT	ACC	ATC	GAT	GCA	AGA	ATG	GTC	GAC	GTA	AAT	GGA	AAA	576
Thr	Val	Asp	Asn	Thr	Ile	Asp	Ala	Arg	Met	Val	Asp	Val	Asn	Gly	Lys	
			180					185						190		
ATT	TTG	GAT	AGA	AAA	TTG	ATG	GGA	GAA	GAT	CTC	TAC	TGG	GCA	ATA	AAC	624
Ile	Leu	Asp	Arg	Lys	Leu	Met	Gly	Glu	Asp	Leu	Tyr	Trp	Ala	Ile	Asn	
		195					200					205				
GGA	GGA	GGA	GGA	GGG	AGC	TAC	GGC	GTC	GTA	TTG	GCC	TAC	AAA	ATA	AAC	672
Gly	Gly	Gly	Gly	Gly	Ser	Tyr	Gly	Val	Val	Leu	Ala	Tyr	Lys	Ile	Asn	
	210					215					220					
CTT	GTT	GAA	GTC	CCA	GAA	AAC	GTC	ACC	GTT	TTC	AGA	ATC	TCC	CGG	ACG	720
Leu	Val	Glu	Val	Pro	Glu	Asn	Val	Thr	Val	Phe	Arg	Ile	Ser	Arg	Thr	
225					230					235					240	
TTA	GAA	CAA	AAT	GCG	ACG	GAT	ATC	ATT	CAC	CGG	TGG	CAA	CAA	GTT	GCA	768
Leu	Glu	Gln	Asn	Ala	Thr	Asp	Ile	Ile	His	Arg	Trp	Gln	Gln	Val	Ala	
			245						250					255		
CCG	AAG	CTT	CCC	GAC	GAG	CTT	TTC	ATA	AGA	ACA	GTC	ATT	GAC	GTA	GTA	816
Pro	Lys	Leu	Pro	Asp	Glu	Leu	Phe	Ile	Arg	Thr	Val	Ile	Asp	Val	Val	
			260					265					270			
AAC	GGC	ACT	GTT	TCA	TCT	CAA	AAG	ACC	GTC	AGG	ACA	ACA	TTC	ATA	GCA	864
Asn	Gly	Thr	Val	Ser	Ser	Gln	Lys	Thr	Val	Arg	Thr	Thr	Phe	Ile	Ala	
		275					280					285				
ATG	TTT	CTA	GGA	GAC	ACG	ACA	ACT	CTA	CTG	TCG	ATA	TTA	AAC	CGG	AGA	912
Met	Phe	Leu	Gly	Asp	Thr	Thr	Thr	Leu	Leu	Ser	Ile	Leu	Asn	Arg	Arg	
	290					295					300					
TTC	CCA	GAA	TTG	GGT	TTG	GTC	CGG	TCT	GAC	TGT	ACC	GAA	ACA	AGC	TGG	960
Phe	Pro	Glu	Leu	Gly	Leu	Val	Arg	Ser	Asp	Cys	Thr	Glu	Thr	Ser	Trp	
305					310					315					320	
ATC	CAA	TCT	GTG	CTA	TTC	TGG	ACA	AAT	ATC	CAA	GTT	GGT	TCG	TCG	GAG	1008
Ile	Gln	Ser	Val	Leu	Phe	Trp	Thr	Asn	Ile	Gln	Val	Gly	Ser	Ser	Glu	
			325					330						335		
ACA	CTT	CTA	CTC	CAA	AGG	AAT	CAA	CCC	GTG	AAC	TAC	CTC	AAG	AGG	AAA	1056
Thr	Leu	Leu	Leu	Gln	Arg	Asn	Gln	Pro	Val	Asn	Tyr	Leu	Lys	Arg	Lys	
			340					345					350			
TCA	GAT	TAC	GTA	CGT	GAA	CCG	ATT	TCA	AGA	ACC	GGT	TTA	GAG	TCA	ATT	1104
Ser	Asp	Tyr	Val	Arg	Glu	Pro	Ile	Ser	Arg	Thr	Gly	Leu	Glu	Ser	Ile	
		355					360					365				
TGG	AAG	AAA	ATG	ATC	GAG	CTT	GAA	ATT	CCG	ACA	ATG	GCT	TTC	AAT	CCA	1152
Trp	Lys	Lys	Met	Ile	Glu	Leu	Glu	Ile	Pro	Thr	Met	Ala	Phe	Asn	Pro	
	370					375					380					

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cont



TAC	GGT	GGT	GAG	ATG	GGG	AGG	ATA	TCA	TCT	ACG	GTG	ACT	CCG	TTC	CCA	1200
Tyr	Gly	Gly	Glu	Met	Gly	Arg	Ile	Ser	Ser	Thr	Val	Thr	Pro	Phe	Pro	
385					390					395					400	
TAC	AGA	GCC	GGT	AAT	CTC	TGG	AAG	ATT	CAG	TAC	GGT	GCG	AAT	TGG	AGA	1248
Tyr	Arg	Ala	Gly	Asn	Leu	Trp	Lys	Ile	Gln	Tyr	Gly	Ala	Asn	Trp	Arg	
			405						410					415		
GAT	GAG	ACT	TTA	ACC	GAC	CGG	TAC	ATG	GAA	TTG	ACG	AGG	AAG	TTG	TAC	1296
Asp	Glu	Thr	Leu	Thr	Asp	Arg	Tyr	Met	Glu	Leu	Thr	Arg	Lys	Leu	Tyr	
			420					425						430		
CAA	TTC	ATG	ACA	CCA	TTT	GTT	TCC	AAG	AAT	CCG	AGA	CAA	TCG	TTT	TTC	1344
Gln	Phe	Met	Thr	Pro	Phe	Val	Ser	Lys	Asn	Pro	Arg	Gln	Ser	Phe	Phe	
		435						440						445		
AAT	TAC	CGT	GAT	GTT	GAT	TTG	GGT	ATT	AAT	TCT	CAT	AAT	GGT	AAA	ATC	1392
Asn	Tyr	Arg	Asp	Val	Asp	Leu	Gly	Ile	Asn	Ser	His	Asn	Gly	Lys	Ile	
		450					455							460		
AGT	AGT	TAT	GTG	GAA	GGT	AAA	CGT	TAC	GGG	AAG	AAG	TAT	TTC	GCA	GGT	1440
Ser	Ser	Tyr	Val	Glu	Gly	Lys	Arg	Tyr	Gly	Lys	Lys	Tyr	Phe	Ala	Gly	
465					470					475					480	
AAT	TTC	GAG	AGA	TTG	GTG	AAG	ATT	AAG	ACG	AGA	GTT	GAT	AGT	GGT	AAT	1488
Asn	Phe	Glu	Arg	Leu	Val	Lys	Ile	Lys	Thr	Arg	Val	Asp	Ser	Gly	Asn	
				485					490					495		
TTC	TTT	AGG	AAC	GAA	CAG	AGT	ATT	CCT	GTG	TTA	CCA	TAA				1527
Phe	Phe	Arg	Asn	Glu	Gln	Ser	Ile	Pro	Val	Leu	Pro					
			500					505								

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Thr	Ser	Arg	Arg	Asn	Ser	Glu	Thr	Phe	Thr	Gln	Cys	Leu	Thr	Ser	Asn	
1				5					10					15		
Ser	Asp	Pro	Lys	His	Pro	Ile	Ser	Pro	Ala	Ile	Phe	Phe	Ser	Gly	Asn	
			20					25					30			
Gly	Ser	Tyr	Ser	Ser	Val	Leu	Gln	Ala	Asn	Ile	Arg	Asn	Leu	Arg	Phe	
		35					40					45				
Asn	Thr	Thr	Ser	Thr	Pro	Lys	Pro	Phe	Leu	Ile	Ile	Ala	Ala	Thr	His	
		50				55					60					
Glu	Ser	His	Val	Gln	Ala	Ala	Ile	Thr	Cys	Gly	Lys	Arg	His	Asn	Leu	
65					70					75					80	

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Gln	Met	Lys	Ile	Arg	Ser	Gly	Gly	His	Asp	Tyr	Asp	Gly	Leu	Ser	Tyr	85	90	95
Val	Thr	Tyr	Ser	Gly	Lys	Pro	Phe	Phe	Val	Leu	Asp	Met	Phe	Asn	Leu	100	105	110
Arg	Ser	Val	Asp	Val	Asp	Val	Ala	Ser	Lys	Thr	Ala	Trp	Val	Gln	Thr	115	120	125
Gly	Ala	Ile	Leu	Gly	Glu	Val	Tyr	Tyr	Tyr	Ile	Trp	Glu	Lys	Ser	Lys	130	135	140
Thr	Leu	Ala	Tyr	Pro	Ala	Gly	Ile	Cys	Pro	Thr	Val	Gly	Val	Gly	Gly	145	150	155
His	Ile	Ser	Gly	Gly	Gly	Tyr	Gly	Asn	Met	Met	Arg	Lys	Tyr	Gly	Leu	165	170	175
Thr	Val	Asp	Asn	Thr	Ile	Asp	Ala	Arg	Met	Val	Asp	Val	Asn	Gly	Lys	180	185	190
Ile	Leu	Asp	Arg	Lys	Leu	Met	Gly	Glu	Asp	Leu	Tyr	Trp	Ala	Ile	Asn	195	200	205
Gly	Gly	Gly	Gly	Gly	Ser	Tyr	Gly	Val	Val	Leu	Ala	Tyr	Lys	Ile	Asn	210	215	220
Leu	Val	Glu	Val	Pro	Glu	Asn	Val	Thr	Val	Phe	Arg	Ile	Ser	Arg	Thr	225	230	235
Leu	Glu	Gln	Asn	Ala	Thr	Asp	Ile	Ile	His	Arg	Trp	Gln	Gln	Val	Ala	245	250	255
Pro	Lys	Leu	Pro	Asp	Glu	Leu	Phe	Ile	Arg	Thr	Val	Ile	Asp	Val	Val	260	265	270
Asn	Gly	Thr	Val	Ser	Ser	Gln	Lys	Thr	Val	Arg	Thr	Thr	Phe	Ile	Ala	275	280	285
Met	Phe	Leu	Gly	Asp	Thr	Thr	Thr	Leu	Leu	Ser	Ile	Leu	Asn	Arg	Arg	290	295	300
Phe	Pro	Glu	Leu	Gly	Leu	Val	Arg	Ser	Asp	Cys	Thr	Glu	Thr	Ser	Trp	305	310	315
Ile	Gln	Ser	Val	Leu	Phe	Trp	Thr	Asn	Ile	Gln	Val	Gly	Ser	Ser	Glu	325	330	335
Thr	Leu	Leu	Leu	Gln	Arg	Asn	Gln	Pro	Val	Asn	Tyr	Leu	Lys	Arg	Lys	340	345	350
Ser	Asp	Tyr	Val	Arg	Glu	Pro	Ile	Ser	Arg	Thr	Gly	Leu	Glu	Ser	Ile	355	360	365
Trp	Lys	Lys	Met	Ile	Glu	Leu	Glu	Ile	Pro	Thr	Met	Ala	Phe	Asn	Pro	370	375	380

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Tyr Gly Gly Glu Met Gly Arg Ile Ser Ser Thr Val Thr Pro Phe Pro  
 385 390 395 400  
 Tyr Arg Ala Gly Asn Leu Trp Lys Ile Gln Tyr Gly Ala Asn Trp Arg  
 405 410 415  
 Asp Glu Thr Leu Thr Asp Arg Tyr Met Glu Leu Thr Arg Lys Leu Tyr  
 420 425 430  
 Gln Phe Met Thr Pro Phe Val Ser Lys Asn Pro Arg Gln Ser Phe Phe  
 435 440 445  
 Asn Tyr Arg Asp Val Asp Leu Gly Ile Asn Ser His Asn Gly Lys Ile  
 450 455 460  
 Ser Ser Tyr Val Glu Gly Lys Arg Tyr Gly Lys Lys Tyr Phe Ala Gly  
 465 470 475 480  
 Asn Phe Glu Arg Leu Val Lys Ile Lys Thr Arg Val Asp Ser Gly Asn  
 485 490 495  
 Phe Phe Arg Asn Glu Gln Ser Ile Pro Val Leu Pro  
 500 505

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana
- (B) STRAIN: Colombia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

TCC ATC CAA GAT CAA TTC ATA AAC TGT GTC AAA AGA AAC ACA CAT GTT 48  
 Ser Ile Gln Asp Gln Phe Ile Asn Cys Val Lys Arg Asn Thr His Val  
 1 5 10 15  
 TCT TTT CCA CTC GAG AAA ACG TTA TTC ACC CCT GCG AAA AAC GTC TCT 96  
 Ser Phe Pro Leu Glu Lys Thr Leu Phe Thr Pro Ala Lys Asn Val Ser  
 20 25 30

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TTG	TTC	AAC	CAA	GTC	CTT	GAA	TCG	ACG	GCT	CAA	AAT	CTC	CAG	TTC	TTG	144
Leu	Phe	Asn	Gln	Val	Leu	Glu	Ser	Thr	Ala	Gln	Asn	Leu	Gln	Phe	Leu	
		35					40					45				
GCA	AAA	TCC	ATG	CCT	AAA	CCG	GGA	TTC	ATA	TTC	AGA	CCG	ATT	CAC	CAG	192
Ala	Lys	Ser	Met	Pro	Lys	Pro	Gly	Phe	Ile	Phe	Arg	Pro	Ile	His	Gln	
	50					55					60					
TCT	CAA	GTC	CAA	GCT	TCC	ATC	ATT	TGT	TCA	AAG	AAA	CTC	GGA	ATT	CAT	240
Ser	Gln	Val	Gln	Ala	Ser	Ile	Ile	Cys	Ser	Lys	Lys	Leu	Gly	Ile	His	
	65				70					75					80	
TTT	CGT	GTT	AGA	AGT	GGC	GGT	CAC	GAT	TTC	GAG	GCC	TTG	TCT	TAT	GTT	288
Phe	Arg	Val	Arg	Ser	Gly	Gly	His	Asp	Phe	Glu	Ala	Leu	Ser	Tyr	Val	
				85				90						95		
TCA	CGG	ATT	GAA	AAA	CCG	TTT	ATA	TTA	CTC	GAC	CTG	TCA	AAA	TTG	AAA	336
Ser	Arg	Ile	Glu	Lys	Pro	Phe	Ile	Leu	Leu	Asp	Leu	Ser	Lys	Leu	Lys	
			100					105					110			
CAA	ATC	AAT	GTT	GAT	ATT	GAA	TCC	AAT	AGT	GCT	TGG	GTT	CAA	CCT	GGT	384
Gln	Ile	Asn	Val	Asp	Ile	Glu	Ser	Asn	Ser	Ala	Trp	Val	Gln	Pro	Gly	
		115					120					125				
GCT	ACG	CTT	GGT	GAG	CTT	TAC	TAC	AGA	ATT	GCA	GAG	AAG	AGC	AAG	ATC	432
Ala	Thr	Leu	Gly	Glu	Leu	Tyr	Tyr	Arg	Ile	Ala	Glu	Lys	Ser	Lys	Ile	
	130					135					140					
CAT	GGA	TTT	CCC	GCG	GGT	TTG	TGC	ACA	AGT	GTA	GGC	ATA	GGT	GGG	TAT	480
His	Gly	Phe	Pro	Ala	Gly	Leu	Cys	Thr	Ser	Val	Gly	Ile	Gly	Gly	Tyr	
	145				150					155					160	
ATG	ACA	GGC	GGT	GGA	TAC	GGT	ACC	TTG	ATG	AGG	AAG	TAT	GGT	CTT	GCG	528
Met	Thr	Gly	Gly	Gly	Tyr	Gly	Thr	Leu	Met	Arg	Lys	Tyr	Gly	Leu	Ala	
				165				170					175			
GGA	GAT	AAT	GTT	CTA	GAC	GTA	AAG	ATG	GTT	GAT	GCA	AAT	GGT	AAA	TTA	576
Gly	Asp	Asn	Val	Leu	Asp	Val	Lys	Met	Val	Asp	Ala	Asn	Gly	Lys	Leu	
			180					185					190			
CTC	GAC	AGA	GCC	GCG	ATG	GGT	GAG	GAC	CTA	TTT	TGG	GCG	ATT	AGA	GGA	624
Leu	Asp	Arg	Ala	Ala	Met	Gly	Glu	Asp	Leu	Phe	Trp	Ala	Ile	Arg	Gly	
		195					200					205				
GGC	GGT	GGA	GCG	AGT	TTC	GGG	ATA	GTT	CTA	GCA	TGG	AAG	ATC	AAG	CTT	672
Gly	Gly	Gly	Ala	Ser	Phe	Gly	Ile	Val	Leu	Ala	Trp	Lys	Ile	Lys	Leu	
	210					215					220					
GTT	CCT	GTT	CCT	AAG	ACT	GTT	ACC	GTC	TTC	ACT	GTC	ACC	AAA	ACG	TTA	720
Val	Pro	Val	Pro	Lys	Thr	Val	Thr	Val	Phe	Thr	Val	Thr	Lys	Thr	Leu	
	225				230					235					240	
GAA	CAA	GAC	GCA	AGA	TTG	AAG	ACT	ATT	TCT	AAG	TGG	CAA	CAA	ATT	TCA	768
Glu	Gln	Asp	Ala	Arg	Leu	Lys	Thr	Ile	Ser	Lys	Trp	Gln	Gln	Ile	Ser	
				245					250					255		

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TCC	AAG	ATT	ATT	GAA	GAG	ATA	CAC	ATC	CGA	GTG	GTA	CTC	AGA	GCA	GCT	816
Ser	Lys	Ile	Ile	Glu	Glu	Ile	His	Ile	Arg	Val	Val	Leu	Arg	Ala	Ala	
			260					265					270			
GGA	AAT	GAT	GGA	AAC	AAG	ACT	GTG	ACA	ATG	ACC	TAC	CTA	GGT	CAG	TTT	864
Gly	Asn	Asp	Gly	Asn	Lys	Thr	Val	Thr	Met	Thr	Tyr	Leu	Gly	Gln	Phe	
			275				280						285			
CTT	GGC	GAG	AAA	GGC	ACC	TTG	CTG	AAG	GTT	ATG	GAG	AAG	GCT	TTT	CCA	912
Leu	Gly	Glu	Lys	Gly	Thr	Leu	Leu	Lys	Val	Met	Glu	Lys	Ala	Phe	Pro	
			290				295						300			
GAA	CTA	GGG	TTA	ACT	CAA	AAG	GAT	TGT	ACT	GAA	ATG	AGC	TGG	ATT	GAA	960
Glu	Leu	Gly	Leu	Thr	Gln	Lys	Asp	Cys	Thr	Glu	Met	Ser	Trp	Ile	Glu	
305					310					315					320	
GCC	GCC	CTT	TTC	CAT	GGT	GGA	TTT	CCA	ACA	GGT	TCT	CCT	ATT	GAA	ATT	1008
Ala	Ala	Leu	Phe	His	Gly	Gly	Phe	Pro	Thr	Gly	Ser	Pro	Ile	Glu	Ile	
				325				330						335		
TTG	CTT	CAG	CTC	AAG	TCG	CCT	CTA	GGA	AAA	GAT	TAC	TTC	AAA	GCA	ACG	1056
Leu	Leu	Gln	Leu	Lys	Ser	Pro	Leu	Gly	Lys	Asp	Tyr	Phe	Lys	Ala	Thr	
			340					345					350			
TCG	GAT	TTC	GTT	AAA	GAA	CCT	ATT	CCT	GTG	ATA	GGC	TTC	AAA	GGA	ATA	1104
Ser	Asp	Phe	Val	Lys	Glu	Pro	Ile	Pro	Val	Ile	Gly	Phe	Lys	Gly	Ile	
		355					360					365				
TTC	AAA	AGA	TTG	ATT	GAA	GGA	AAC	ACA	ACA	TTT	CTG	AAC	TGG	ACT	CCT	1152
Phe	Lys	Arg	Leu	Ile	Glu	Gly	Asn	Thr	Thr	Phe	Leu	Asn	Trp	Thr	Pro	
		370				375					380					
TAC	GGT	GGT	ATG	ATG	TCG	AAA	ATC	CCT	GAA	TCT	GCG	ATC	CCA	TTT	CCG	1200
Tyr	Gly	Gly	Met	Met	Ser	Lys	Ile	Pro	Glu	Ser	Ala	Ile	Pro	Phe	Pro	
385					390					395				400		
CAT	AGA	AAC	GGA	ACC	CTC	TTC	AAG	ATT	CTC	TAT	TAC	GCG	AAC	TGG	CTA	1248
His	Arg	Asn	Gly	Thr	Leu	Phe	Lys	Ile	Leu	Tyr	Tyr	Ala	Asn	Trp	Leu	
				405					410					415		
GAG	AAT	GAC	AAG	ACA	TCG	AGT	AGA	AAA	ATC	AAC	TGG	ATC	AAA	GAG	ATA	1296
Glu	Asn	Asp	Lys	Thr	Ser	Ser	Arg	Lys	Ile	Asn	Trp	Ile	Lys	Glu	Ile	
			420					425					430			
TAC	AAT	TAC	ATG	GCG	CCT	TAT	GTC	TCA	AGC	AAT	CCA	AGA	CAA	GCA	TAT	1344
Tyr	Asn	Tyr	Met	Ala	Pro	Tyr	Val	Ser	Ser	Asn	Pro	Arg	Gln	Ala	Tyr	
			435				440					445				
GTG	AAC	TAC	AGA	GAT	CTA	GAC	TTC	GGA	CAG	AAC	AAG	AAC	AAC	GCA	AAG	1392
Val	Asn	Tyr	Arg	Asp	Leu	Asp	Phe	Gly	Gln	Asn	Lys	Asn	Asn	Ala	Lys	
			450			455					460					
GTT	AAC	TTC	ATT	GAA	GCT	AAA	ATC	TGG	GGA	CCT	AAG	TAC	TTC	AAA	GGC	1440
Val	Asn	Phe	Ile	Glu	Ala	Lys	Ile	Trp	Gly	Pro	Lys	Tyr	Phe	Lys	Gly	
465					470					475				480		
AAT	TTT	GAC	AGA	TTG	GTG	AAG	ATT	AAA	ACC	AAG	GTT	GAT	CCA	GAG	AAC	1488
Asn	Phe	Asp	Arg	Leu	Val	Lys	Ile	Lys	Thr	Lys	Val	Asp	Pro	Glu	Asn	
				485					490					495		

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Cont

TTC TTC AGG CAC GAG CAG AGT ATC CCA CCT ATG CCC TAC TAG  
Phe Phe Arg His Glu Gln Ser Ile Pro Pro Met Pro Tyr  
500 505

1530

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Ser Ile Gln Asp Gln Phe Ile Asn Cys Val Lys Arg Asn Thr His Val  
1 5 10 15

Ser Phe Pro Leu Glu Lys Thr Leu Phe Thr Pro Ala Lys Asn Val Ser  
20 25 30

Leu Phe Asn Gln Val Leu Glu Ser Thr Ala Gln Asn Leu Gln Phe Leu  
35 40 45

Ala Lys Ser Met Pro Lys Pro Gly Phe Ile Phe Arg Pro Ile His Gln  
50 55 60

Ser Gln Val Gln Ala Ser Ile Ile Cys Ser Lys Lys Leu Gly Ile His  
65 70 75 80

Phe Arg Val Arg Ser Gly Gly His Asp Phe Glu Ala Leu Ser Tyr Val  
85 90 95

Ser Arg Ile Glu Lys Pro Phe Ile Leu Leu Asp Leu Ser Lys Leu Lys  
100 105 110

Gln Ile Asn Val Asp Ile Glu Ser Asn Ser Ala Trp Val Gln Pro Gly  
115 120 125

Ala Thr Leu Gly Glu Leu Tyr Tyr Arg Ile Ala Glu Lys Ser Lys Ile  
130 135 140

His Gly Phe Pro Ala Gly Leu Cys Thr Ser Val Gly Ile Gly Gly Tyr  
145 150 155 160

Met Thr Gly Gly Gly Tyr Gly Thr Leu Met Arg Lys Tyr Gly Leu Ala  
165 170 175

Gly Asp Asn Val Leu Asp Val Lys Met Val Asp Ala Asn Gly Lys Leu  
180 185 190

Leu Asp Arg Ala Ala Met Gly Glu Asp Leu Phe Trp Ala Ile Arg Gly  
195 200 205

Gly Gly Gly Ala Ser Phe Gly Ile Val Leu Ala Trp Lys Ile Lys Leu  
210 215 220

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Val Pro Val Pro Lys Thr Val Thr Val Phe Thr Val Thr Lys Thr Leu  
 225 230 235 240  
 Glu Gln Asp Ala Arg Leu Lys Thr Ile Ser Lys Trp Gln Gln Ile Ser  
 245 250 255  
 Ser Lys Ile Ile Glu Glu Ile His Ile Arg Val Val Leu Arg Ala Ala  
 260 265 270  
 Gly Asn Asp Gly Asn Lys Thr Val Thr Met Thr Tyr Leu Gly Gln Phe  
 275 280 285  
 Leu Gly Glu Lys Gly Thr Leu Leu Lys Val Met Glu Lys Ala Phe Pro  
 290 295 300  
 Glu Leu Gly Leu Thr Gln Lys Asp Cys Thr Glu Met Ser Trp Ile Glu  
 305 310 315 320  
 Ala Ala Leu Phe His Gly Gly Phe Pro Thr Gly Ser Pro Ile Glu Ile  
 325 330 335  
 Leu Leu Gln Leu Lys Ser Pro Leu Gly Lys Asp Tyr Phe Lys Ala Thr  
 340 345 350  
 Ser Asp Phe Val Lys Glu Pro Ile Pro Val Ile Gly Phe Lys Gly Ile  
 355 360 365  
 Phe Lys Arg Leu Ile Glu Gly Asn Thr Thr Phe Leu Asn Trp Thr Pro  
 370 375 380  
 Tyr Gly Gly Met Met Ser Lys Ile Pro Glu Ser Ala Ile Pro Phe Pro  
 385 390 395 400  
 His Arg Asn Gly Thr Leu Phe Lys Ile Leu Tyr Tyr Ala Asn Trp Leu  
 405 410 415  
 Glu Asn Asp Lys Thr Ser Ser Arg Lys Ile Asn Trp Ile Lys Glu Ile  
 420 425 430  
 Tyr Asn Tyr Met Ala Pro Tyr Val Ser Ser Asn Pro Arg Gln Ala Tyr  
 435 440 445  
 Val Asn Tyr Arg Asp Leu Asp Phe Gly Gln Asn Lys Asn Asn Ala Lys  
 450 455 460  
 Val Asn Phe Ile Glu Ala Lys Ile Trp Gly Pro Lys Tyr Phe Lys Gly  
 465 470 475 480  
 Asn Phe Asp Arg Leu Val Lys Ile Lys Thr Lys Val Asp Pro Glu Asn  
 485 490 495  
 Phe Phe Arg His Glu Gln Ser Ile Pro Pro Met Pro Tyr  
 500 505

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